

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:26:58 ; Search time 11.7455 Seconds
(without alignments)
933.402 Million cell updates/sec

Title: US-10-027-725A-7

Perfect score: 609

Sequence: 1 LESGRLVKNPQTLISLSCAV.....RLDGYTLIDMGQGLTVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	479.5	78.7	116	2 S37456	Ig mu chain - huma
2	476.5	78.2	135	2 S78051	Ig heavy chain pre
3	475.5	78.1	128	2 S31514	Ig heavy chain - h
4	465	76.4	122	2 S69912	Ig V-D-J region (N
5	464.5	76.3	147	2 S13519	Ig heavy chain V r
6	460	75.5	130	2 S30534	Ig heavy chain V r
7	458.5	75.3	140	2 I37782	Ig variable region
8	453	74.4	99	2 S26801	Ig heavy chain V r
9	452.5	74.3	146	2 S09710	Ig heavy chain V r
10	451.5	74.1	121	2 S44113	Ig heavy chain V r
11	451.5	74.1	130	2 S31690	Ig heavy chain V r
12	450.5	74.0	127	2 S15668	Ig heavy chain V r
13	449.5	73.8	146	2 S09711	Ig heavy chain - h
14	449.5	73.8	155	2 S31511	Ig heavy chain - h
15	446.5	73.3	155	2 S31512	Ig heavy chain - h
16	444	72.9	137	2 S31676	Ig heavy chain V r
17	440	72.2	139	2 S31586	Ig heavy chain V r
18	439	72.1	145	2 S78055	Ig heavy chain pre
19	436	71.6	99	2 S26803	Ig heavy chain V r
20	435.5	71.5	123	2 S30530	Ig heavy chain V r
21	434	71.3	129	2 S44114	Ig heavy chain V r
22	433.5	71.2	117	2 E34964	Ig heavy chain pre
23	432.5	71.0	109	2 PH1673	Ig heavy chain V r
24	431	70.8	99	2 S26802	Ig heavy chain V r
25	430	70.6	97	2 PLO118	Ig heavy chain V-I
26	427	70.1	99	2 S26899	Ig heavy chain V-I
27	427	70.1	110	2 S44110	Ig heavy chain V-D
28	426	70.0	139	2 A41287	Ig heavy chain pre
29	425.5	69.9	121	2 C55257	Ig gamma heavy cha

30	424	69.6	118	2 A26340	Ig heavy chain pre
31	423	69.5	118	2 S20780	Ig heavy chain V r
32	421.5	69.2	140	2 A49045	Ig heavy chain V r
33	419.5	68.9	129	1 D2HWA	Ig heavy chain V-I
34	419	68.8	135	2 S31604	Ig heavy chain V r
35	418.5	68.7	132	2 A38911	Ig heavy chain V r
36	418	68.6	99	2 S26807	Ig heavy chain V r
37	417	68.5	115	2 S57464	Ig heavy chain V-J
38	417	68.5	126	2 S47010	Ig heavy chain V4.
39	417	68.5	140	2 S78052	Ig heavy chain pre
40	416.5	68.4	140	2 A24770	Ig heavy chain pre
41	415.5	68.2	143	2 B49028	Ig heavy chain V-I
42	415	68.1	99	2 S12418	Ig heavy chain V r
43	414.5	68.0	137	2 S31585	Ig heavy chain V r
44	414	68.0	120	2 PR0370	Ig mu chain precu
45	412.5	67.7	98	2 S26902	Ig heavy chain V r

ALIGNMENTS

```
RESULT 1
S37456
Ig mu chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37456
R:McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A:Description: Cloning and analysis of human Igm anti-rhryoglobulin autoantibodies from
A:Reference number: S37453
A:Accession: S37456
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <MC1>
A:Cross-references: EMBL:X75024; NID:G40413; PIDN:CA452932.1; PID:G758095
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F/6-90/Domain: immunoglobulin homology <IMM>

Query Match          78.7%; Score 479.5; DB 2; Length 116;
Best Local Similarity 76.1%; Pred. No. 4.6e-38;
Matches 89; Conservative 14; Mismatches 5; Indels 9; Gaps 2;

QY      6 GIVKPAQTLSICAVSGSISGYYMSWIKQHPKGLGEMIGYIHSNTYINPSLKSR 65
      |||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 GIVKPSQTLSTLCTVSGSISGYYMSWIKQHPKGLGEMIGYIHSNTYINPSLKSRV 60
QY      66 AMSVDTSENKPSLRINSVTADPTAVYYCARLDGYT-----LDIMGQGLTVTVSS 114
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      61 TISVDTSNQPSLKLISVTADPTAVYYCAR-GGISYGYIYYIMDVWGKGLTVTVSS 116

RESULT 2
S78051
Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78051; S23716
R:Haridranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78051
A:Molecule type: mRNA
A:Residues: 1-135 <HAR>
A:Cross-references: EMBL:X54437; NID:G37814; PIDN:CA438306.1; PID:G930117
R:Haridranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
  Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the VH and VL regions of low- and h
  patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404
A:Accession: S23716
A:Molecule type: mRNA
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OM protein - protein search, using sw model

Run on: February 10, 2004, 17:48:48 : Search time 6.39091 Seconds
(without alignments)
838.855 Million cell updates/sec

Title: US-10-027-725A-7

Sequence: 1 LESGPGLVKPAQTLSLSCAV.....RLDGYTLIDMGQGLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	419.5	68.9	129	1	HY2F_HUMAN
2	405	66.5	126	1	HY2I_HUMAN
3	374.5	61.5	137	1	HY46_MOUSE
4	369.5	60.7	117	1	HY2G_HUMAN
5	361.5	59.4	113	1	HY47_MOUSE
6	342.5	56.2	116	1	HY61_MOUSE
7	341.5	56.1	116	1	HY60_MOUSE
8	334	54.8	117	1	HY62_MOUSE
9	321.5	52.8	144	1	HY43_MOUSE
10	304	49.9	135	1	HY02_XENLA
11	300	49.3	120	1	HY2B_HUMAN
12	295	48.4	119	1	HY40_MOUSE
13	293	48.1	122	1	HY3A_HUMAN
14	288	47.3	119	1	HY38_MOUSE
15	285.5	46.9	119	1	HY2C_HUMAN
16	285	46.8	119	1	HY37_MOUSE
17	282.5	46.4	121	1	HY3J_HUMAN
18	280.5	46.1	117	1	HY2B_RABIT
19	278.5	45.7	125	1	HY2D_HUMAN
20	276	45.3	114	1	HY3B_HUMAN
21	275	45.2	122	1	HY3G_HUMAN
22	274.5	45.1	121	1	HY2E_HUMAN
23	274	45.0	116	1	HY05_CARAU
24	273	44.8	122	1	HY3H_HUMAN
25	272	44.7	114	1	HY2A_RABIT
26	272	44.7	122	1	HY2I_MOUSE
27	271	44.5	147	1	HY2H_HUMAN
28	270.5	44.4	115	1	HY3F_HUMAN
29	270.5	44.4	117	1	HY4I_MOUSE
30	270	44.3	115	1	HY44_MOUSE
31	270	44.3	122	1	HY20_MOUSE
32	269.5	44.3	142	1	HY01_RAT
33	268.5	44.1	115	1	HY3D_HUMAN

34	268.5	44.1	117	1	HY42_MOUSE	P01812 mus musculus
35	267.5	43.9	117	1	HY12_MOUSE	P01756 mus musculus
36	267.5	43.9	123	1	HY25_MOUSE	P01794 mus musculus
37	267	43.8	116	1	HY45_MOUSE	P01821 mus musculus
38	267	43.8	126	1	HY2A_HUMAN	P01814 homo sapien
39	267	43.8	139	1	HY07_MOUSE	P01751 mus musculus
40	266.5	43.8	117	1	HY13_MOUSE	P01757 mus musculus
41	266.5	43.8	118	1	HY33_MOUSE	P01809 mus musculus
42	266.5	43.8	123	1	HY22_MOUSE	P01791 mus musculus
43	265.5	43.6	123	1	HY18_MOUSE	P01787 mus musculus
44	265.5	43.6	123	1	HY19_MOUSE	P01788 mus musculus
45	264.5	43.4	123	1	HY24_MOUSE	P01793 mus musculus

ALIGNMENTS

RESULT 1

ID HY2F_HUMAN STANDARD; PRT; 129 AA.

AC P01824; 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP MEDLINE=8222235; PubMed=606818;
RX Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
PROTEIN.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2HWA.
DR HSSP; P01825; 7PAB.
DR GLYcositedB; P01824; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 113 IG-LIKE.
FT NON TER 129
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 68.9%; Score 419.5; DB 1; Length 129;
Best local similarity 62.7%; Pred. No. 3.5e-38;
Matches 79; Conservative 16; Mismatches 16; Indels 15; Gaps 2;

QY	2	ESGPGVPAQTLSLSCAVSGSIRSGGYSWIRHFGKGLKEMIGTYHSGNRYNSL	61
DB	6	ESGPGVPAQTLSLSCAVSGSIRSGGYSWIRHFGKGLKEMIGTYHSGNRYNSL	65
QY	62	KSRIAMSVDSENFSEFLNSVTAADTAIVVYCAR-----LDGYTLIDMGQGT	108
DB	66	RGRTIVSDIVSRNPFSLNLSMSAADTAMVYCAAGNPPYDICTGSDG--IDVGGGT	123
QY	109	LVTYSS 114	
DB	124	TVHYSS 129	

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RESULT 2
HV21_HUMAN
ID HV21_HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85205332; PubMed=3922855;
RA Kudo A., Ishihara T., Nishimura Y., Matanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT repeat sequence in 5' flanking region."
RL Gene 33:181-189 (1985).
DR PIR: A02101; GIHM2.
DR HSSP: P01825; 7PAB.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.
FT DOMAIN 20 117 V SEGMENT.
FT DOMAIN 118 127 D SEGMENT.
FT DOMAIN 128 146 J SEGMENT.
FT DISULFID 42 115 BY SIMILARITY.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match 66.5%; Score 405; DB 1; Length 146;
Best Local Similarity 66.9%; Pred. No. 1,4e-36;
Matches 81; Conservative 13; Mismatches 15; Indels 12; Gaps 3;

QY 4 GPGLVKPAQTLSGCAVSGSGISGQYWMIRQPKGLEWYGYIHSNTYTNLSLKS 63
DB |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
28 GAGLVKPSERTSLTCAVFGGSF--SGYWMIRQPKGLEWYGYIHSNTYTNLSLKS 85
QY 64 RIMASVDTSENKPSLRNSTYTAADTAVYYCAR--LDG-----YTLDIWGQGLVTVS 113
DB |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
86 RVTISLDTSKNLSLKLSTYTAADTAVYYCARGLRGRANDVDYYIGMDVWGQGLTVTVS 145
QY 114 S 114
DB | 146 S 146

RESULT 3
HV46_MOUSE
ID HV46_MOUSE STANDARD; PRT; 137 AA.
AC P01852;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain V region MOPC 315 precursor.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89238351; PubMed=2497341;
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;

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RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
RT gene segment."
RL Mol. Immunol. 26:431-434 (1989).
RN [2]
RX SEQUENCE OF 1-31.
RX MEDLINE=78094475; PubMed=414225;
RA Jilka R.L., Peetka S.;
RT "Amino acid sequence of the precursor region of MOPC-315 mouse
RT immunoglobulin heavy chain."
RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).
RN [3]
RP SEQUENCE OF 1-21.
RX MEDLINE=79148758; PubMed=428562;
RA Schechter I., Wolf O., Zemell R., Burestein Y.;
RT "Structure and function of immunoglobulin genes and precursors."
RL Fed. Proc. 38:1835-1845 (1979).
RN [4]
RP SEQUENCE OF 19-136.
RX MEDLINE=74170779; PubMed=4524622;
RA Francis S.H., Leslie R.G.O., Hood L., Eisen H.N.;
RT "Amino-acid sequence of the variable region of the heavy (alpha)
RT chain of a mouse myeloma protein with anti-hapten activity."
RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127 (1974).
RN [5]
RP REVISION TO 53.
RX MEDLINE=77244979; PubMed=268248;
RA Hood L., Margolies M.N., Givol D., Zakut R.;
RL Unpublished results, cited by:
RL Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637 (1977).
CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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CC EMBL; M27638; AAA61337.1; -
CC EMBL; X07880; CAA30727.1; -
DR PIR: P0102; AVM835.
DR HSSP: P01825; 7PAB.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003066; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IGV_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
KW
FT SIGNAL 1 18
FT CHAIN 19 137 IG HEAVY CHAIN V REGION MOPC 315.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 86 FRAMEWORK-3.
FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 127 137 FRAMEWORK-4.
FT DISULFID 40 114 BY SIMILARITY.
FT CONFLICT 15 15 G->G (IN REF. 1; CAA30727).
FT CONFLICT 15 15 G->H (IN REF. 2).
FT CONFLICT 77 78 G->Y (IN REF. 4).
FT CONFLICT 102 102 N->D (IN REF. 4).
FT CONFLICT 123 123 MISSING (IN REF. 4).
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;

Query Match 61.5%; Score 374.5; DB 1; Length 137;
Best Local Similarity 61.7%; Pred. No. 2,6e-33;
Matches 71; Conservative 20; Mismatches 21; Indels 3; Gaps 2;

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OY 2 ESGGGLVPAQTLTSLSCAVSGGSTRSGGYWMTROHPGKLEWIGYTHSGNTYVPSL 61
DB 24 ESGGGLVPSQSLSITCSVTYSITS-GYFNNWTRQPGNKLEWIGYTHSGNTYVPSL 82
OY 62 KSRJAMSVDTSSENFSLRLNSVTADTAVYYCARLDG--YTLDIWGQGLTVTVSS 114
DB 63 KNRVITRDTISENPFKLNSVTEDTATYTCAGDNHLYFDYWGQGLTVTVSS 137

RESULT 4
HV2G HUMAN STANDARD; PRT; 117 AA.
AC P01825;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region NEMM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77242302; PubMed=407927;
RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
RT "Amino acid sequence of the VH region of a human myeloma
immunoglobulin (IgG New).";
RL Biochemistry 16:3412-3420(1977).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
RX MEDLINE=78066916; PubMed=618887;
RA Saul P.A., Anzel L.M., Poljak R.J.;
RT "Preliminary refinement and structural analysis of the Fab fragment
from human immunoglobulin new at 2.0-A resolution.";
RL J. Biol. Chem. 253:585-597(1978).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGSI MYELOMA
PROTEIN.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90404; G1HNM.
DR PDB; 7PAB; 31-JAN-94.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
FT DOMAIN 1 111
FT MOD_RES 1 1
FT STRAND 3 7
FT TURN 11 12
FT TURN 14 15
FT STRAND 18 25
FT TURN 30 31
FT STRAND 33 39
FT TURN 41 42
FT STRAND 46 51
FT TURN 53 54
FT STRAND 57 59
FT HELIX 61 63
FT TURN 64 66
FT STRAND 67 72
FT TURN 73 76
FT STRAND 77 82
FT HELIX 87 89
FT STRAND 91 98
FT STRAND 104 107
FT STRAND 111 115
FT NON_TER 117

SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;
Query Match 60.7%; Score 369.5; DB 1; Length 117;
Best Local Similarity 61.4%; Pred. No. 7,4e-33;
Matches 70; Conservative 22; Mismatches 19; Indels 3; Gaps 2;
OY 2 ESGGGLVPAQTLTSLSCAVSGGSTRSGGYWMTROHPGKLEWIGYTHSGNTYVPSL 61
DB 6 ESGGGLVPSQSLSITCSVTYSITS-GYFNNWTRQPGNKLEWIGYTHSGNTYVPSL 82
OY 62 KSRJAMSVDTSSENFSLRLNSVTADTAVYYCARLDG--YTLDIWGQGLTVTVSS 114
DB 64 KSRVITRDTISENPFKLNSVTEDTATYTCAGDNHLYFDYWGQGLTVTVSS 137

RESULT 5
HV47 MOUSE STANDARD; PRT; 113 AA.
AC P01823;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-60.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX STRAIN=A/J;
RC MEDLINE=84024551; PubMed=6414509;
RA Juszczak E.C., Margolies M.N.;
RT "Amino acid sequence of the heavy chain variable region from the A/J
mouse anti-arsenate monoclonal antibody 36-60 bearing a minor
idiotype.";
RL Biochemistry 22:4291-4296(1983).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIRASONATE
MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND
IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIRASONATE RESPONSE OF
STRAIN A/J MICE.
CC CC
DR PIR; A02098; G2MS60.
DR PDB; 1J10; 18-FEB-03.
DR PDB; 1J1P; 18-FEB-03.
DR PDB; 1J1X; 18-FEB-03.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; 3D-structure.
FT NON_TER 113
SQ SEQUENCE 113 AA; 12734 MW; 38DC0E3F5075B7 CRC64;
Query Match 59.4%; Score 361.5; DB 1; Length 113;
Best Local Similarity 62.8%; Pred. No. 5,1e-32;
Matches 71; Conservative 18; Mismatches 19; Indels 5; Gaps 2;
OY 2 ESGGGLVPAQTLTSLSCAVSGGSTRSGGYWMTROHPGKLEWIGYTHSGNTYVPSL 61
DB 6 ESGGGLVPSQSLSITCSVTYSITS-GYFNNWTRQPGNKLEWIGYTHSGNTYVPSL 82
OY 62 KSRJAMSVDTSSENFSLRLNSVTADTAVYYCARLDG--YTLDIWGQGLTVTVSS 114
DB 64 KSRVITRDTISENPFKLNSVTEDTATYTCAGDNHLYFDYWGQGLTVTVSS 137

RESULT 6
HV61 MOUSE STANDARD; PRT; 116 AA.
AC P18532;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 1B43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
DR PIR; J0508; HWSJ1B.
DR PDB; 1KCV; 11-MAY-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION 1B43.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 67 FRAMEWORK-2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON TER 116 116
SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681F74 CRC64;

Query Match 56.1%; Score 342.5; DB 1; Length 116;
Best Local Similarity 69.1%; Pred. No. 5.9e-30;
Matches 65; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

QY 2 ESGPGLVVKPAQTLISLCAVSGSIRSGGYWMSIRHQPCKGLEWIGYIHSGNTYYPSTL 61
DB 24 ESGPGLVVKPQSLSLCTCTVGTGYSITS-GYWMHWRQFPCKLEWIGYIHSGNTYYPSTL 82
QY 62 KSRIMSVDTSENKFSRLNSVTADTAATVYCAR 95
DB 83 KSRISTRTDTSKNQFPLKNSVTTEDTATVYCAR 116

RESULT 7
H60 MOUSE STANDARD; PRT; 116 AA.
ID HV60_MOUSE
AC P18531;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region M315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
DR PIR; J0509; HWSJ1.
DR HSSP; J01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 117 IG HEAVY CHAIN V REGION 733.
FT DOMAIN 19 53
FT DOMAIN 49 67
FT DOMAIN 54 67
FT DOMAIN 68 84
FT DOMAIN 85 116
FT DISULFID 40 114
FT NON TER 117 117 BY SIMILARITY.
SQ SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;

Query Match 54.8%; Score 334; DB 1; Length 117;
Best Local Similarity 64.9%; Pred. No. 4.9e-29;
Matches 61; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 2 ESGPGLVVKPAQTLISLCAVSGSIRSGGYWMSIRHQPCKGLEWIGYIHSGNTYYPSTL 61
DB 24 ESGPGLVVKPQSLSLCTCTVGTGYSITS-GYWMHWRQFPCKLEWIGYIHSGNTYYPSTL 83

DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION M315.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 67 FRAMEWORK-2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON TER 116 116
SQ SEQUENCE 116 AA; 13095 MW; 4562E03E53DC9E10 CRC64;

Query Match 56.1%; Score 341.5; DB 1; Length 116;
Best Local Similarity 67.0%; Pred. No. 7.5e-30;
Matches 63; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

QY 2 ESGPGLVVKPAQTLISLCAVSGSIRSGGYWMSIRHQPCKGLEWIGYIHSGNTYYPSTL 61
DB 24 ESGPGLVVKPQSLSLCTCTVGTGYSITS-GYWMHWRQFPCKLEWIGYIHSGNTYYPSTL 82
QY 62 KSRIMSVDTSENKFSRLNSVTADTAATVYCAR 95
DB 83 KSRISTRTDTSKNQFPLKNSVTTEDTATVYCAR 116

RESULT 8
H62 MOUSE STANDARD; PRT; 117 AA.
ID HV62_MOUSE
AC P18533;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 733 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; J0510; HWSJ73.
DR HSSP; J01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 117 IG HEAVY CHAIN V REGION 733.
FT DOMAIN 19 53
FT DOMAIN 49 67
FT DOMAIN 54 67
FT DOMAIN 68 84
FT DOMAIN 85 116
FT DISULFID 40 115
FT NON TER 117 117 BY SIMILARITY.
SQ SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;

Query Match 54.8%; Score 334; DB 1; Length 117;
Best Local Similarity 64.9%; Pred. No. 4.9e-29;
Matches 61; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 2 ESGPGLVVKPAQTLISLCAVSGSIRSGGYWMSIRHQPCKGLEWIGYIHSGNTYYPSTL 61
DB 24 ESGPGLVVKPQSLSLCTCTVGTGYSITS-GYWMHWRQFPCKLEWIGYIHSGNTYYPSTL 83

QY 62 KSRIAMSVDTSENKESRLNSVTADTAVYYCAR 95
 DB 84 KSRITTRDTSKNOFPLENNSLTADTAVYYCAR 117

RESULT 9
 HY43_MOUSE
 ID_HV43_MOUSE STANDARD; PRT; 144 AA.

AC P01819;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MOPC 141 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]

SEQUENCE FROM N.A.
 RX MEDLINE=81012133; PubMed=6774258;
 RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
 RT "Two types of somatic recombination are necessary for the generation
 of complete immunoglobulin heavy-chain genes.";
 RL Nature 286:676-683(1980).
 CC -1- MICRILANOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
 DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
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 CC -----
 CC EMBL; V00768; CA24149.1; -
 DR PIR; A02094; G2MS14.
 DR HSSP; P01825; 7FAB.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.
 FT DOMAIN 20 130 IG-LIKE.
 FT NON_TER 144 144
 FT SEQUENCE 144 AA; 15759 MW; 8E47A7CEB3706D30A CRC64;

Query Match 52.8%; Score 321.5; DB 1; Length 144;
 Best Local Similarity 54.1%; Pred. No. 1.4e-27;
 Matches 66; Conservative 21; Mismatches 24; Indels 11; Gaps 3;

QY 2 ESGPGLVPAQTLTSLCAVSGSIRSGGYMSWIRQHPGKLEWIGIYHSGNTYVPSL 61
 DB 25 ESGPGLVPAQSLTITCTYSGFSLT--GYGVNVMVQPPKGLGEMIGTIMGNSTYVPSL 82

QY 62 KSRIAMSVDTSENKESRLNSVTADTAVYYCAR-----RLDGY-TLTDWGQGLTVV 112
 DB 83 KSRITTRDTSKNOFPLENNSLTADTAVYYCASVSIYYGRSDKXFTLDWGQGLTVV 142

QY 113 SS 114
 DB 143 SS 144

RESULT 10
 HY02_XENLA
 ID_HY02_XENLA STANDARD; PRT; 135 AA.

AC P20957;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region XIG14 precursor (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8335;
 RN [1]

SEQUENCE FROM N.A.
 RX MEDLINE=88176921; PubMed=2451244;
 RA Schwager J., Mikoyak C.A., Steiner L.A.;
 RT "Amino acid sequence of heavy chain for evolution of immunoglobulin
 from cDNA sequence: implications for evolution of immunoglobulin
 domains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J03632; AAA49791.1; -
 DR PIR; B31933; B31933.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT NON_TER 1 1
 FT SIGNAL 1 18
 FT CHAIN 19 135 IG HEAVY CHAIN V REGION XIG14.
 FT DOMAIN 20 128 IG-LIKE.
 FT NON_TER 135 135
 FT SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Query Match 49.9%; Score 304; DB 1; Length 135;
 Best Local Similarity 51.3%; Pred. No. 9.7e-26;
 Matches 59; Conservative 19; Mismatches 33; Indels 4; Gaps 2;

QY 2 ESGPGLVPAQTLTSLCAVSGSIRSGGYMSWIRQHPGKLEWIGIYHSGNTYVPSL 61
 DB 23 ESGPGLVPAQSLTITCTYSGFELSS--YHNMWIRQHPGKLEWIGIYATGSTRADSL 80

QY 62 KSRIAMSVDTSENKESRLNSVTADTAVYYCAR--LDGYTLTDWGQGLTVVSS 114
 DB 81 KSRITTRDTSKNOFPLENNSLTADTAVYYCASVSIYYGRSDKXFTLDWGQGLTVVSS 135

RESULT 11
 HY2B_HUMAN
 ID_HY2B_HUMAN STANDARD; PRT; 120 AA.

AC P01815;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region COR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]

SEQUENCE
 RX MEDLINE=70258837; PubMed=5449120;

RA Press E.M., Hogg N.M.;
 RT "The amino acid sequences of the Fd fragments of two human gamma-1
 heavy chains".
 RL Biochem. J. 117:641-660(1970).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02089; GIHUCO.
 DR HSSP: P01825; 7FAB.
 DR GO: GO:0005576; Extracellular; NAS.
 DR GO: GO:0003823; Antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 110
 FT MOD RES 1 110
 FT DISULFID 22 94
 FT CARBOHYD 62 62
 FT NON TER 120 120
 FT SEQUENCE 120 AA; 13226 MW; 158A8B29A87EB98 CRC64;
 SQ
 Query Match 49.3%; Score 300; DB 1; Length 120;
 Best Local Similarity 52.9%; Pred. No. 2.3e-25;
 Matches 63; Conservative 16; Mismatches 30; Indels 10; Gaps 3;
 QY 2 ESPPGVVPAQNTLSLCAVSGSIRSGGYWMSIRHPGKGLMIGIYHSGNTYNPST 61
 DB 6 EESPPALVKPTGITLTCTSGFSLSTGKCVGMIKRPFGKGLMIRIMDDDKYINTSI 65
 QY 62 KSRIANSVDTSENKFSRLNSVTADTAVYYCARLD-----GYTLDMGQGLVTSS 114
 DB 66 ETRLTISKDTSRNQVVLTMPPV---DTATYCARITVTPAPAGY-MDVWGRTPTVYSS 120
 RESULT 12
 ID HVA0 MOUSE STANDARD; PRT; 119 AA.
 AC P01810;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ig heavy chain V region J539.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN (1)
 RP PRELIMINARY SEQUENCE.
 RX MEDLINE=79223895; PubMed=111245;
 RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
 RT "Structural evidence for independent joining region gene in
 immunoglobulin heavy chains from anti-galactan myeloma proteins and
 its potential role in generating diversity in
 complementarity-determining regions.";
 RT Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979).
 RL [2]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=88217852; PubMed=3449853;
 RA Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
 RA Davies D.R.;
 RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
 study at 2.6-A resolution.";
 RL Proteins 1:74-80(1986).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 BINDS GALACTAN.
 CC PIR: A02080; AVMSJ5.
 CC PDB: 2FAB; 15-OCT-90.
 DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; IGV; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; 3D-structure.
 FT STRAND 3 7
 FT NON TER 119 119
 FT TURN 10 12
 FT TURN 14 15
 FT STRAND 18 15
 FT STRAND 18 25
 FT HELIX 29 31
 FT STRAND 34 39
 FT TURN 41 42
 FT STRAND 45 51
 FT TURN 53 54
 FT TURN 58 60
 FT TURN 62 67
 FT STRAND 68 72
 FT STRAND 78 83
 FT HELIX 88 90
 FT STRAND 92 100
 FT TURN 101 103
 FT STRAND 104 108
 FT STRAND 112 116
 FT SEQUENCE 119 AA; 13240 MW; 577B4F1DB675C1F1 CRC64;
 SQ
 Query Match 48.4%; Score 295; DB 1; Length 119;
 Best Local Similarity 53.4%; Pred. No. 7.8e-25;
 Matches 62; Conservative 16; Mismatches 34; Indels 4; Gaps 3;
 QY 1 LESGGLVPAQNTLSLCAVSGSIRSGGYWMSIRHPGKGLMIGIYHSGNTYNPST 59
 DB 5 LESGGGLVDPGSGSLKLSCAVSGFDPK--YMSWVRQAPGKGLMIGIHPGSGINTYPT 62
 QY 60 SKSRIANSVDTSENKFSRLNSVTADTAVYYCARLDGYTLDMGQGLVTSS 114
 DB 63 SLKDFIISRDNAKNSLYLQMSKVRSEPTALYYCARLHYGYNAVYGGTGLVTSSA 118
 RESULT 13
 ID HVA3 HUMAN STANDARD; PRT; 122 AA.
 AC P01762;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-III region TRO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE (MYELOMA PROTEIN TRO).
 RX MEDLINE=76023781; PubMed=809331;
 RA Kratzin H., Altevogt P., Ruban E., Kortt A., Starosck K.,
 RA Hilschmann N.;
 RT "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.),
 RT II. The amino acid sequence of the H-chain, alpha-type, subgroup III;
 RT structure of the complete IgA-molecule.";
 RL Hoppe-Seiler's Z. Physiol. Chem. 356:1337-1342(1975).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02045; A1HTR.
 DR HSSP: P01772; 2F84.
 DR GO: GO:0005576; Extracellular; NAS.
 DR GO: GO:0003823; Antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; IGV; 1.
 DR SMART: SM00406; IGV; 1.

DR PROSITE: PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Pyroliidone carboxylic acid.
 FT DOMAIN 1 108
 FT MOD RES 1 1 PYROLIDONE CARBOXYLIC ACID.
 FT NON TER 122 122
 SQ SEQUENCE 122 AA; 13472 MW; 2B21A11DA04D80F9 CRC64;

Query Match 48.1%; Score 293; DB 1; Length 122;
 Best Local Similarity 47.5%; Pred. No. 1.3e-24;
 Matches 57; Conservative 21; Mismatches 34; Indels 8; Gaps 3;

QY 1 LESGGLVPAQTLISCAVSGSIRSGGYWMIROHPKGLKLEWIGYIYHSGNTY-YNP 59
 DB 5 VQSGGGLVPGGSLRLSCVAASFGRD--PYMSWIRZIRPGKGLZMVSYIIGSGSLTYTAD 62
 QY 60 SLKSRIVMSVDTSEKFSRLNSVTADTAVYVCALDQ---YTLDIWGGTLVTSS 114
 DB 63 SVKGRFTISRDAKQSLYLZMBSLRTZBTAVYVCATBFBWSTFSLBYMGZGLVTSS 122

RESULT 14
 HV38 MOUSE STANDARD; PRT; 119 AA.
 AC P01808;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DE Ig heavy chain V region T601.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxId=10090;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=79223895; PubMed=111245;
 RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
 RT "Structural evidence for independent joining region gene in
 immunoglobulin heavy chains from anti-galactan myeloma proteins and
 its potential role in generating diversity in
 RT complementarity-determining regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
 CC THAT BINDS GALACTAN.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02078; AWMST6.
 DR HSSP: P01810; 2F8J.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 112
 FT NON TER 119 119 IG-LIKE.
 SQ SEQUENCE 119 AA; 13169 MW; BC38C84BEAD0E8 CRC64;

Query Match 47.3%; Score 288; DB 1; Length 119;
 Best Local Similarity 52.6%; Pred. No. 4.4e-24;
 Matches 61; Conservative 15; Mismatches 36; Indels 4; Gaps 3;

QY 1 LESGGLVPAQTLISCAVSGSIRSGGYWMIROHPKGLKLEWIGYIYHSGNTY-YNP 59
 DB 5 LESGGLVPGGSLRLSCVAASFGRD--SRVMSWVQAPGKGLKLEWIGYIYHSGNTY 62
 QY 60 SLKSRIVMSVDTSEKFSRLNSVTADTAVYVCALDQ---YTLDIWGGTLVTSS 114
 DB 63 SLKDXFTISRDAKQSLYLZMBSLRTZBTAVYVCATBFBWSTFSLBYMGZGLVTSS 118

RESULT 15
 HV2C HUMAN STANDARD; PRT; 119 AA.
 ID HV2C_HUMAN

AC P01816;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DE Ig heavy chain V-II region DAM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_TaxId=9606;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=70258837; PubMed=5449120;
 RA Press E.M., Hogg N.M.;
 RT "The amino acid sequences of the Fd fragments of two human gamma-1
 RT heavy chains.";
 RL Biochem. J. 117:641-660(1970).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE
 CC SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02091; G1HDPW.
 DR HSSP: P01789; IMCP.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Pyroliidone carboxylic acid.
 FT DOMAIN 1 113
 FT NON TER 119 119 PYROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;

Query Match 46.9%; Score 285.5; DB 1; Length 119;
 Best Local Similarity 50.9%; Pred. No. 8.2e-24;
 Matches 58; Conservative 18; Mismatches 37; Indels 1; Gaps 1;

QY 2 ESGGLVPAQTLISCAVSGSIRSGGYWMIROHPKGLKLEWIGYIYHSGNTYNSL 61
 DB 6 ESGGLVPAQTLISCAVSGSIRSGGYWMIROHPKGLKLEWIGYIYHSGNTYNSL 65
 QY 62 KSRIAMSVDTSEKFSRLNSVTADTAVYVCALDQ---YTLDIWGGTLVTSS 114
 DB 66 ETRILAVSKDTSKNOVLSMTVPGDPTATYVCARSCSQYFDYWGGLVTSS 119

Search completed: February 10, 2004, 18:36:29
 Job time : 6.39091 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	451	74.1	150	4	Q95973	Q95973 homo sapien
2	446.5	73.3	119	4	Q9ULI73	Q9ULI73 homo sapien
3	432	70.9	496	4	Q96KX8	Q96KX8 homo sapien
4	430	70.6	613	4	Q96EY0	Q96EY0 homo sapien
5	409.5	67.2	588	4	Q8WUX4	Q8WUX4 homo sapien
6	409.5	67.2	597	4	Q9BU10	Q9BU10 homo sapien
7	409.5	67.2	618	4	Q96KA6	Q96KA6 homo sapien
8	405.5	66.6	597	4	Q98BD8	Q98BD8 homo sapien
9	405	66.5	130	4	Q81XD7	Q81XD7 homo sapien
10	388	63.7	473	4	Q8T6C3	Q8T6C3 homo sapien
11	377.5	62.0	479	11	Q99M22	Q99M22 mus musculus
12	362	59.4	122	4	Q9ULI75	Q9ULI75 homo sapien
13	323	53.0	121	11	Q99NG4	Q99NG4 mus musculus
14	316.5	52.0	121	4	Q9UI96	Q9UI96 homo sapien
15	315	51.7	482	11	Q91IX2	Q91IX2 mus musculus
16	312.5	51.3	118	4	Q9ULI74	Q9ULI74 homo sapien

17	300	49.3	613	4	Q8MU1	Q8mu1 homo sapien
18	295.5	48.5	113	4	Q9U190	Q9u190 homo sapien
19	295.5	48.5	116	4	Q9U193	Q9u193 homo sapien
20	295	48.4	118	4	Q9U172	Q9u172 homo sapien
21	293.5	48.2	597	4	Q96BB9	Q96bb9 homo sapien
22	292	47.9	118	4	Q9U191	Q9u191 homo sapien
23	290.5	47.7	493	4	Q8NCL6	Q8nc16 homo sapien
24	285	46.8	471	4	Q8TC77	Q8tc77 homo sapien
25	284.5	46.7	121	4	Q9UL71	Q9ul71 homo sapien
26	284	46.6	484	11	Q8VEA0	Q8vea0 mus musculus
27	282.5	46.4	119	5	Q9GYR2	Q9gyr2 schistosoma
28	282.5	46.4	481	11	Q91WT1	Q91wt1 mus musculus
29	282	46.3	145	11	Q92AR1	Q92ar1 mus musculus
30	281.5	46.2	499	4	Q8NSK4	Q8nsk4 homo sapien
31	281	46.1	122	4	Q9UL84	Q9ul84 homo sapien
32	281	46.1	573	4	Q8MU38	Q8mu38 homo sapien
33	280	46.0	469	11	Q8R3V9	Q8r3v9 mus musculus
34	279	45.8	145	11	Q924P7	Q924p7 mus musculus
35	278	45.6	147	4	Q9Y509	Q9y509 homo sapien
36	277	45.5	124	6	Q9N0W6	Q9n0w6 oryctolagus
37	277	45.5	298	11	Q9QTF0	Q9qtf0 mus musculus
38	277	45.5	494	4	Q96K68	Q96k68 homo sapien
39	276.5	45.4	117	11	Q9QXE9	Q9qxe9 mus musculus
40	276	45.3	112	4	Q9HCC1	Q9hcc1 homo sapien
41	276	45.3	124	6	Q9N0M4	Q9n0m4 oryctolagus
42	275	45.2	143	11	Q924R0	Q924r0 mus musculus
43	274	45.0	145	11	Q924R4	Q924r4 mus musculus
44	273.5	44.9	117	11	Q9QXFR	Q9qxfr mus musculus
45	272.5	44.7	480	11	Q91XE1	Q91xe1 mus musculus

ALIGNMENTS

QY	2	ESGGLYKPAQTLSLSCAVSGSGIRSGGYWSWRHDPGKGLFWYIYHSGNRYNPSTL	61
Query Match	74.1%	Score 451; DB 4; Length 150;	
Best Local Similarity	74.3%;	Pred. No. 9.1e-40;	
Matches 84;	Conservative 12;	Mismatches 17; Indels 0; Gaps 0;	

[illegible]

RESULT 2

ID	OSUL73	PRELIMINARY;	PRT;	119 AA.
AC	OSUL73;			
DT	01-MAY-2000 (TrEMBLrel, 13, Created)			
DT	01-MAY-2000 (TrEMBLrel, 13, last sequence update)			
DT	01-MAR-2003 (TrEMBLrel, 23, last annotation update)			
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment).			
DE	Homo sapiens (human).			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			

RT	CLIN.	Immunol.	Immunopathol.	87:184-192(1996).
RT	ferus."			
RA	Young D.C.;			
RA	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,			
RF	MEDLINE=98277139;			
RF	SEQUENCE FROM N.A.			
Q	SEQUENCE	119 AA,	13219 MW,	1BD86B6420EAOBE CRC64;
FT	NON_TER	1	119	
DR	PROSITE	PS50835;	IG LIKE,	1.
DR	SMART	SM00406;	IGV,	1.
DR	PIfam	PF00047;	IG,	1.
DR	InterPro	IPR003596;	IG_V,	
DR	InterPro	IPR003006;	IG_MHC,	
DR	InterPro	IPR007110;	IG-like,	
DR	HSPSP	P01825;	7PAB.	
DR	EMBL	AF035041;	AA256277.1;	-.
RL				

Query Match	73.3%	Score	446.5	DB	4	Length	119
Best Local Similarity	74.1%	Pred. No.	26-35				
Matches	86	Conservative	12	Mismatches	13	Indels	5
						Gaps	2

Qy 2 EESGGLVKPQPTTSLSCAVSGSGSTRSQGGYWSWRHDPGKGLKWTGYTHSGNTYTNPSL 6
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 6 EESGGLVKPSTSLSLTCTVSGSGICS--YMSWRDPGKGLKWTGYTHSSGNTNTPSL 6
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 62 KSRITAMSDVTSSEKFSRLNLSVTADPAAVYICARLDC---YTLDDIKGGSTLTVYSS 114
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 64 KSRITATSDRSKDNFSLKTLSTLTADPAAVYFCALSLNMGPEYDFYQGGTLTVYSS 119
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 3

ID	096KX8	PRELIMINARY;	PRT;	496 AA.
AC	Q96KX8			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE	Hypotheoretical protein.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_			
RP	SEQUENCE FROM N.A.			
RC				
RF	TISSUE=Lung;			
RA	Strausberg R.;			
RL	Submitted (OCCT-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC016369; AAL16369.1; -			
DR	InterPro; IPR007110; IG_11ke.			
DR	InterPro; IPR003006; IG_MHC.			

DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS00290; IG_MHC; 1.
DR KQ Hypothetical protein.
QW SEQUENCE 46 AA; 53391 MW; D3469298A9040D69 CRC64

[illegible]

RESULT 4

ID	PRELIMINARY	PRT	613 AA
AC	Q96EY0		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	Hypothetical protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
NCBI_TaxID=9606;			

RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases
DR EMBL; BC011857; AAH11857.1; -
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR pfam; PF00047; Ig_5.
DR SMART; SM00406; IGV_1.
DR PROSITE; PSS0835; IG_LITE; 5.
DR PROSITE; PSS00290; IG_MHC; 3.
KM Hypothetical protein.
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match	70.6%	Score 430	DB 4	Length 613
Best Local Similarity	74.4%	Pred. No. 8.9e-37		
Matches 87	Conservative	9	Mismatches 15	Indels 6
				Gaps 2

Oy 2 ESAGGLVAPQOTLISLCAVSGGSIIRGGGYWMSIRHPPKGLEMIYTHSGNTVNSPL 6
::: ::::: :
Dd 25 ESRGGLVKPESFTLSLTIVSGGSISS--YMSIIRQPKAGLEMIGRITSSGTNNPSL 8
:
Oy 62 KSRIANSVDTSSENKFSRLNLSVTAAADTAVYYCA----RLDGYLLDIWGQTLTVTSS 114
::: ::::: :
Ib 83 KSRITVNSVDTSNKQFSLKLKLSVTAAADTAVYYCASQPELPTVGALFYWGQTLTVTSS 139
::: ::::: :

RESULT 5

ID	NAME	PRELIMINARY	PRT.	588-AA.
AC	OSMIX4			
AC	OSMIX4			
DT	01-MAR-2002 (T-EMBLrel. 20, Created)			
DT	01-MAR-2002 (T-EMBLrel. 20, Last sequence update)			
DT	01-MAR-2003 (T-EMBLrel. 23, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strauberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019235; AAH19235.1; -
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 588 AA; 64438 MW; FC60BAD82B39FD7 CRC64;

Query Match 67.2%; Score 409.5; DB 4; Length 588;
 Best Local Similarity 66.7%; Pred. No. 1.2e-34;
 Matches 80; Conservative 14; Mismatches 15; Indels 11; Gaps 3;

Oy 4 GPGLVKPAQTLISLCAVSGSIRSGGYWSWIRQHPGKLEWIGYIHSGNTYNSPLKS 63
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 27 GAGLKPSETLSLTCGVYGGSF--SGYWSWIRQHPGKLEWIGYIHSGNTYNSPLKS 84
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Oy 64 RIAMSVDTSENKFSRLNSVTAADTAAYYCARL-----DG-YTLDIWGQGLTVTVSS 114
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 85 RVTISVDTSKKQLSLKSSVNAADTAAYYCARVITRASPGTDGRYGMVWGQGLTVTVSS 144

RESULT 6

O9BU10 PRELIMINARY; PRT; 597 AA.
 ID O9BU10
 AC O9BU10;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strauberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002963; AAH02963.1; -
 DR HSSP; P01825; 7FAB.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 67.2%; Score 409.5; DB 4; Length 597;
 Best Local Similarity 66.7%; Pred. No. 1.3e-34;
 Matches 80; Conservative 14; Mismatches 15; Indels 11; Gaps 3;

Oy 4 GPGLVKPAQTLISLCAVSGSIRSGGYWSWIRQHPGKLEWIGYIHSGNTYNSPLKS 63
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 27 GAGLKPSETLSLTCGVYGGSF--SGYWSWIRQHPGKLEWIGYIHSGNTYNSPLKS 84
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Oy 64 RIAMSVDTSENKFSRLNSVTAADTAAYYCARL-----DG-YTLDIWGQGLTVTVSS 114
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 85 RVTISVDTSKKQLSLKSSVNAADTAAYYCARVITRASPGTDGRYGMVWGQGLTVTVSS 144

RESULT 7

O96AA6 PRELIMINARY; PRT; 618 AA.
 ID O96AA6
 AC O96AA6;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strauberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC017356; AAH17356.1; -
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;

Query Match 67.2%; Score 409.5; DB 4; Length 618;
 Best Local Similarity 66.7%; Pred. No. 1.3e-34;
 Matches 80; Conservative 14; Mismatches 15; Indels 11; Gaps 3;

Oy 4 GPGLVKPAQTLISLCAVSGSIRSGGYWSWIRQHPGKLEWIGYIHSGNTYNSPLKS 63
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 27 GAGLKPSETLSLTCGVYGGSF--SGYWSWIRQHPGKLEWIGYIHSGNTYNSPLKS 84
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Oy 64 RIAMSVDTSENKFSRLNSVTAADTAAYYCARL-----DG-YTLDIWGQGLTVTVSS 114
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 85 RVTISVDTSKKQLSLKSSVNAADTAAYYCARVITRASPGTDGRYGMVWGQGLTVTVSS 144

RESULT 8

O9BOB8 PRELIMINARY; PRT; 597 AA.
 ID O9BOB8
 AC O9BOB8;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle, and Lymph;
 RA Strauberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006180; AAH06180.1; -
 DR EMBL; BC001872; AAH01872.1; -
 DR HSSP; P01825; 7FAB.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 66.6%; Score 405.5; DB 4; Length 597;
 Best Local Similarity 66.7%; Pred. No. 3.3e-34;
 Matches 80; Conservative 13; Mismatches 16; Indels 11; Gaps 3;


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OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035039; AAD56275.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; I9_1like.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_v.
DR Pfam; PF00047; I9; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; I9_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 122 AA; 13719 MW; 56CB0612586A6529 CRC64;

Query Match 59.4%; Score 362; DB 4; Length 122;
Best Local Similarity 61.9%; Pred. No. 1.7e-30;
Matches 73; Conservative 15; Mismatches 24; Indels 6; Gaps 3;

QY 2 ESGPGLVPAQTLSLSCAVSGSIRSGGYWSMIRHKGKLEWIGYTHSGNTY--YNP 59
DB 6 QSGPGLVPSQTLTLTCAISGDSVSSNSAMWNIQSPSRGLEWIGRTYYSKWYNDRV 65

RESULT 13
QY 60 SLKSIAMSVPTSEKFSRLNSVTADTAVYYCAR---LDGYTDINGQGLTVYSS 114
DB 66 SVKSRITINPTISKQVFLQNSVTPEDTAVYYCARDLELG-QDYNGQGLTVYSS 122

Q99NG4 PRELIMINARY; PRT; 121 AA.
ID Q99NG4
AC Q99NG4
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Placental PHENI.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=98169018; PubMed=9510199;
RA Hawisch H., Frank R., Hennecke M., Baensch M., Soehn B., Arseniev L.,
RT Bausch W., Kola A., Klos A., Koehl J.;
RT "Site-directed C3a-Receptor Antibodies from Phage Display Libraries.";
RL J. Immunol. 160:2947-2958(1998).
DR EMBL; AJ222590; CAA10890.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; I9_1like.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_v.
DR Pfam; PF00047; I9; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; I9_LIKE; 1.
DR Plasmid.
KW NON_TER 1
KW NON_TER 1
SQ SEQUENCE 121 AA; 13255 MW; D293B4B8C8C59D5B CRC64;

Query Match 53.0%; Score 323; DB 11; Length 121;
Best Local Similarity 54.7%; Pred. No. 2.2e-26;
Matches 64; Conservative 19; Mismatches 28; Indels 6; Gaps 2;

QY 2 ESGPGLVPAQTLSLSCAVSGSIRSGGYWSMIRHKGKLEWIGYTHSGNTYNSL 61

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DB 6 ESGPGLVAPSGSLISITCTVSGFPLTSHGV--SWVRQPPGKGLVWLGVYWGDKTKYHSAL 63

QY 62 KSRIRASVDTSEKFSRLNSVTADTAVYYCAR---LDGYTDINGQGLTVYSS 114
DB 64 ISRLISKDMSKQVFLKNSLQTEDTAVYYCAHRYKANYAMDYWGQGLTVYSS 120

RESULT 14
Q9UL96 PRELIMINARY; PRT; 121 AA.
ID Q9UL96
AC Q9UL96
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035018; AAD56254.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; I9_1like.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_v.
DR Pfam; PF00047; I9; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; I9_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDJ35 CRC64;

Query Match 52.0%; Score 316.5; DB 4; Length 121;
Best Local Similarity 54.3%; Pred. No. 1.1e-25;
Matches 63; Conservative 14; Mismatches 36; Indels 3; Gaps 1;

QY 2 ESGPGLVPAQTLSLSCAVSGSIRSGGYWSMIRHKGKLEWIGYTHSGNTYNSL 61
DB 6 ESGPGLVXPTQTTLTCTFSGFSLTSGMDVGMWIRPPGKLEWILALTYMDDKRYGPSL 65

QY 62 KSRIRASVDTSEKFSRLNSVTADTAVYYCARL---DGYTDINGQGLTVYSS 114
DB 66 KSRITIKDTSKQVFLQNSVTPEDTAVYYCAHRSKSGDGYFPYWGQGLTVYSS 121

RESULT 15
Q91X92 PRELIMINARY; PRT; 482 AA.
ID Q91X92
AC Q91X92
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Unknown (Protein for WGC:18822).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Straubeberg R.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011181; AAH11181.1; -.
DR InterPro; IPR007110; I9_1like.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:32:44 : Search time 11.7455 Seconds
(without alignments)
410.664 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614

Sequence: 1 LBSGPGVKKPSQTLSTCTV.....RSDGVTIDNMCGTIVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	507	82.6	473	US-09-049-672A-4	Sequence 4, Appli
2	494	80.5	122	US-08-360-125-11	Sequence 11, Appl
3	494	80.5	122	US-08-450-578-11	Sequence 11, Appl
4	494	80.5	122	US-09-017-628-11	Sequence 11, Appl
5	494	80.5	122	US-09-014-880-11	Sequence 11, Appl
6	494	80.5	122	US-08-450-363-11	Sequence 11, Appl
7	488.5	79.6	119	US-09-025-769B-39	Sequence 39, Appl
8	488.5	79.6	119	US-09-025-769B-65	Sequence 65, Appl
9	488	79.5	118	US-09-025-769B-25	Sequence 25, Appl
10	473.5	77.1	119	US-08-360-125-5	Sequence 5, Appli
11	473.5	77.1	119	US-08-450-578-5	Sequence 5, Appli
12	473.5	77.1	119	US-09-017-628-5	Sequence 5, Appli
13	473.5	77.1	119	US-09-014-880-5	Sequence 5, Appli
14	473.5	77.1	119	US-08-450-363-5	Sequence 5, Appli
15	459.5	74.8	142	US-08-480-774A-2	Sequence 2, Appli
16	458.5	74.7	250	US-10-039-785-50	Sequence 50, Appl
17	458	74.6	244	US-08-918-148-79	Sequence 79, Appl
18	453	73.8	118	US-08-545-809A-116	Sequence 116, App
19	453	73.8	126	US-08-276-852-142	Sequence 142, App
20	453	73.8	126	US-08-899-575-142	Sequence 142, App
21	453	73.8	126	US-08-899-575-142	Sequence 142, App
22	453	73.8	126	PCT-US95-08743-142	Sequence 142, App
23	446.5	72.7	119	US-08-652-816A-10	Sequence 10, Appl
24	446	72.6	118	US-08-545-809A-123	Sequence 123, App
25	446	72.6	278	US-09-260-527-3	Sequence 3, Appli
26	445.5	72.6	123	US-08-793-450-4	Sequence 4, Appli
27	445.5	72.6	472	US-08-793-450-8	Sequence 8, Appli

28	445	72.5	118	US-09-343-698-6	Sequence 6, Appli
29	443	72.1	118	US-08-545-809A-142	Sequence 142, App
30	441	71.8	244	US-10-039-785-44	Sequence 44, Appl
31	440.5	71.7	124	US-08-478-039-78	Sequence 78, Appl
32	440.5	71.7	124	US-08-476-349A-78	Sequence 78, Appl
33	439.5	71.6	126	US-08-487-550-12	Sequence 12, Appl
34	439.5	71.6	476	US-09-526-098-12	Sequence 12, Appl
35	439	71.5	118	US-08-652-816A-13	Sequence 13, Appl
36	438	71.3	832	US-08-630-820-7	Sequence 7, Appli
37	436.5	71.1	219	US-09-460-384-37	Sequence 37, Appl
38	434.5	70.8	123	US-08-137-117D-64	Sequence 64, Appl
39	434.5	70.8	123	US-08-436-717-64	Sequence 64, Appl
40	434.5	70.8	138	US-08-137-117D-69	Sequence 69, Appl
41	434.5	70.8	138	US-08-436-717-69	Sequence 69, Appl
42	432.5	70.4	98	US-08-478-039-75	Sequence 75, Appl
43	432.5	70.4	98	US-08-476-349A-75	Sequence 75, Appl
44	431.5	70.3	121	US-08-275-053-13	Sequence 13, Appl
45	431	70.2	120	US-08-057-430A-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-049-672A-4
Sequence 4, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Yang, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049, 672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ceirone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PR-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANCYTUT01

CLONE: 1513264
US-09-049-672A-4

Query Match 82.6%; Score 507; DB 3; Length 473;
Best Local Similarity 79.8%; Pred. No. 6e-43;
Matches 95; Conservative 9; Mismatches 9; Indels 6; Gaps 1;

QY 2 ESGPGIVKPSQTLTCTVSGSIRSGGYMSVROPPGKGLWIGINIVHSGNTYNNPSL 61
DB 25 ESGPGIVKPSQTLTCTVSGSIRSGGYMSVROPPGKGLWIGINIVHSGNTYNNPSL 84

QY 62 KSRITWSVDTSKNHFSLRLTSVTAADTAVYYCARSD-----GYTLDNWGQGLVTVSS 114
DB 85 KSRITWSVDTSKNHFSLRLTSVTAADTAVYYCARSDVGLRGNGYGMVWGQGLVTVSS 143

RESULT 2
US-08-360-125-11
Sequence 11, Application US/08360125
Patent No. 5767246

GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246hiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSER: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:
HABIT TYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLER:
LIBRARY:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-11

Query Match 80.5%; Score 494; DB 1; Length 122;
Best Local Similarity 78.6%; Pred. No. 2.4e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGPGIVKPSQTLTCTVSGSIRSGGYMSVROPPGKGLWIGINIVHSGNTYNNPSL 61
DB 6 ESGPGIVKPSQTLTCTVSGSIRSGGYMSVROPPGKGLWIGINIVHSGNTYNNPSL 65

QY 62 KSRITWSVDTSKNHFSLRLTSVTAADTAVYYCARSD-----GYTLDNWGQGLVTVSS 114
DB 66 KSRITWSVDTSKNHFSLRLTSVTAADTAVYYCARSDYGGYGMVWGQGLVTVSS 122

RESULT 3
US-08-450-578-11
Sequence 11, Application US/08450578
Patent No. 5837845

GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845hiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSER: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578

;; FILING DATE: May 25, 1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/360,125
;; FILING DATE: December 20, 1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/905,534
;; FILING DATE: June 29, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek, Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX:
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 122 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHEetical:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE: Hybridoma producing human antibody 1-3-1
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-11

Query Match 80.5%; Score 494; DB 2; Length 122;
Best Local Similarity 78.6%; Pred. No. 2.4e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGPGLVPSQTLSTCTVSGSGSISGGYYSWVRQPPGKLEWIGNTYHSGNTYVPSL 61
DB 6 ESGPGLVPSQTLSTCTVSGSGSISGGYYSWVRQPPGKLEWIGNTYHSGNTYVPSL 65

QY 62 KSRITMSVDTSKNHFSLRLTSTVTAADTAIVYYCARSD---GYTLDNWGQGLTVTVSS 114
DB 66 KSRVITISVDTSKNHFSLRLTSTVTAADTAIVYYCARSGYGGYTGMDVWGQGLTVTVSS 122

RESULT 4
US-09-017-628-11
; Sequence 11, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: TAGAWA, Toshiaki
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITO, No. 5990287hiko
; APPLICANT: NAGAIKE, Kazuhiko
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; FILE REFERENCE: 177/527361KH
; CURRENT APPLICATION NUMBER: US/09/017,628
; CURRENT FILING DATE: 1998-02-02
; EARLIER APPLICATION NUMBER: 08/360,125
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-11

Query Match 80.5%; Score 494; DB 2; Length 122;
Best Local Similarity 78.6%; Pred. No. 2.4e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGPGLVPSQTLSTCTVSGSGSISGGYYSWVRQPPGKLEWIGNTYHSGNTYVPSL 61
DB 6 ESGPGLVPSQTLSTCTVSGSGSISGGYYSWVRQPPGKLEWIGNTYHSGNTYVPSL 65

QY 62 KSRITMSVDTSKNHFSLRLTSTVTAADTAIVYYCARSD---GYTLDNWGQGLTVTVSS 114
DB 66 KSRVITISVDTSKNHFSLRLTSTVTAADTAIVYYCARSGYGGYTGMDVWGQGLTVTVSS 122

RESULT 5
US-09-014-880-11
; Sequence 11, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000
 TELEFAX: (212)596-9090
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 118 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-025-769B-25

Query Match 79.5%; Score 488; DB 4; Length 118;
 Best Local Similarity 81.7%; Pred. No. 9.3e-42;
 Matches 94; Conservative 7; Mismatches 10; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYYMSWROPFGKLEWIGNIYHSNTYNNPSL 61
 DB 6 ESGPGLVKPSQTLSTCTVSGSIS--YMSWIRQPGKLEWIGIYHSNTYNNPSL 63
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCA--RSDGTTLDNMGCGTLVTYSS 114
 DB 64 KSRVITSLDTSKNHFSLRLTSVTAADTAVYYCARGRGGGVFDYWGCGTLVTYSS 118

RESULT 10

US-08-360-125-5
 Sequence 5, Application US/08360125
 Patent No. 5767246

GENERAL INFORMATION:

APPLICANT: Saiko HOSOKAWA
 APPLICANT: Tochiaki TAGAWA
 APPLICANT: Yoko HIRAKAWA
 APPLICANT: No. 5767246hiko ITO
 APPLICANT: Kazuhiro NAGAIKE
 TITLE OF INVENTION: Human Monoclonal Antibody
 TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
 TITLE OF INVENTION: Cell Membrane
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wenderoch, Lind & Ponack
 STREET: 805 Fifteenth Street, N.W., #700
 City: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/360,125
 FILING DATE:

CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/905,534
 FILING DATE: June 29, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.
 REGISTRATION NUMBER: 33,367
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-8850
 TELEFAX:

TELEX:
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein
 HYPOTHEICAL:
 AMTI-SENSE:
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM:

STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:

CELL TYPE: Hybridoma producing human
 CELL LINE: antibody GAH
 ORGANELER:

IMMEDIATE SOURCE:

LIBRARY:
 CLONE:
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT:
 MAP POSITION:

UNITS:
 FEATURE:

NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 PUBLICATION INFORMATION:
 AUTHORS:

TITLE:
 JOURNAL:
 VOLUME:
 ISSUE:
 PAGES:

DATE:
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
 US-08-360-125-5

Query Match 77.1%; Score 473.5; DB 1; Length 119;
 Best Local Similarity 78.1%; Pred. No. 2.7e-40;
 Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYYMSWROPFGKLEWIGNIYHSNTYNNPSL 61
 DB 6 ESGPGLVKPSQTLSTCTVSGSIS8CGFYMWIRQPGKLEWIGIYHSNTYNNPSL 65
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYT-LDNMGCGTLVTYSS 114
 DB 66 KSRVITSLDTSKNHFSLRLTSVTAADTAVYYCARSTRLRGADYWGCGTLVTYSS 119

RESULT 11

US-08-450-578-5
 Sequence 5, Application US/08450578
 Patent No. 5837845

GENERAL INFORMATION:

APPLICANT: Saiko HOSOKAWA
 APPLICANT: Tochiaki TAGAWA
 APPLICANT: Yoko HIRAKAWA
 APPLICANT: No. 5837845hiko ITO
 APPLICANT: Kazuhiro NAGAIKE
 TITLE OF INVENTION: Human Monoclonal Antibody
 TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
 TITLE OF INVENTION: Cell Membrane
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wenderoch, Lind & Ponack
 STREET: 805 Fifteenth Street, N.W., #700
 City: Washington

```

Query Match      77.1%; Score 473.5; DB 2; Length 119;
Best Local Similarity 78.1%; Pred. No. 2,7e-40;
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

Cy      2  ESGGVLKPSQTLSTLCTVSGSGSIRSGGYWMSWVRQPPGKLEWIGNIYHSGNTYNPSTL 61
Db      6  ESGGVLKPSQTLSTLCTVSGSGSISCGFYWMNRQHPGKLEWIGIYVSGSTYNPSTL 65

Cy      62 KSRITMSVDTSKNHFSLRLTSVTAADPAVYVCARSDGYT-LDNMGQGLTVTVSS 114
Db      66 KSRVITSLDTSKSFSLKLSLTAADPAVYVCARSTRLRGADYWGQGTMTVTVSS 119

RESULT 12
US-09-017-628-5
; Sequence 5, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: TAGAMA, Toshiaki
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITO, No. 5990287ihiko
; APPLICANT: NAGAIKE, Kazuhiko
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; FILE REFERENCE: 177/527361KH
; CURRENT APPLICATION NUMBER: US/09/017.628
; CURRENT FILING DATE: 1998-02-02
; EARLIER APPLICATION NUMBER: 08/360,125
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-5

Query Match      77.1%; Score 473.5; DB 2; Length 119;
Best Local Similarity 78.1%; Pred. No. 2,7e-40;
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

Cy      2  ESGGVLKPSQTLSTLCTVSGSGSIRSGGYWMSWVRQPPGKLEWIGNIYHSGNTYNPSTL 61
Db      6  ESGGVLKPSQTLSTLCTVSGSGSISCGFYWMNRQHPGKLEWIGIYVSGSTYNPSTL 65

Cy      62 KSRITMSVDTSKNHFSLRLTSVTAADPAVYVCARSDGYT-LDNMGQGLTVTVSS 114
Db      66 KSRVITSLDTSKSFSLKLSLTAADPAVYVCARSTRLRGADYWGQGTMTVTVSS 119

RESULT 13
US-09-014-880-5
; Sequence 5, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS

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SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human
US-09-014-880-5

Query Match 77.1%; Score 473.5; DB 2; Length 119;
Best local Similarity 78.1%; Pred. No. 2.7e-40;
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;
QY 2 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWROPKGLGEMIGNITHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWROPKGLGEMIGNITHSGNTYNNPSL 65
QY 62 KSRITMSVDTSKXHFSLRTSVTAADTAAYVYCARSDGYT-LDNMGQGLTVTVSS 114
DB 66 KSRVITSLDTSKQFSLKLSLTAADTAAYVYCARSTRIRLRGADYWGQGTMTVTVSS 119

RESULT 14
US-08-450-363-5
Sequence 5, Application US/08450363
Patent No. 6436434
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toohiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 6436434hiko ITO
APPLICANT: Kazuhito NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
SPECIFICALLY BINDING TO Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,363
FILING DATE: May 25, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-5

Query Match 77.1%; Score 473.5; DB 4; Length 119;
Best local Similarity 78.1%; Pred. No. 2.7e-40;
Matches 89; Conservative 13; Mismatches 11; Indels 1; Gaps 1;
QY 2 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWROPKGLGEMIGNITHSGNTYNNPSL 61
DB 6 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWROPKGLGEMIGNITHSGNTYNNPSL 65

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 17:46:18 ; Search time 34.3727 Seconds
(without alignments)
526.430 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614
Sequence: 1 LBSGPGLVKESQTLSTCTV.....RSDGYTLDMGQGLTVVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

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1	614	100.0	114	23	ABG30446
2	608	99.0	114	23	ABG30447
3	546	88.9	114	23	ABG30445
4	507	82.6	473	22	AA836206
5	502.5	81.8	123	20	AAW78433
6	502.5	81.8	123	23	ABB97976
7	501	81.6	252	23	ABP45318
8	500.5	81.5	127	22	AA880217
9	500	81.4	126	21	AA830584

10	500	81.4	126	23	ABP54970
11	500	81.4	251	23	ABG80712
12	500	81.4	254	23	ABG80713
13	500	81.4	263	23	ABG80714
14	499.5	81.4	120	22	AA862775
15	498	81.1	123	21	AA862745
16	496.5	80.9	122	22	AA862765
17	496	80.8	246	21	AA85126
18	495	80.6	118	20	AA86385
19	494.5	80.5	251	24	ABJ19829
20	494	80.5	172	21	AA893713
21	493	80.3	252	23	ABP45983
22	492.5	80.2	251	23	ABP44979
23	492.5	80.2	253	23	ABP45608
24	490.5	79.9	117	21	AA844615
25	488.5	79.6	119	18	AAW27554
26	488.5	79.6	119	20	ABJ18676
27	488	79.5	118	20	AA86383
28	488	79.5	139	21	AA856713
29	487	79.3	130	23	AA81273
30	487	79.3	254	23	ABP45567
31	487	79.3	256	23	ABP45596
32	484	78.8	117	22	AA802540
33	484	78.8	122	14	AA830145
34	483.5	78.7	129	23	AA81275
35	483	78.7	229	21	AA830593
36	482	78.5	120	22	AA866415
37	482	78.5	121	23	AB80711
38	482	78.5	146	24	ABP57361
39	482	78.5	154	24	ABP57365
40	480	78.2	250	23	ABP45537
41	479.5	78.1	129	23	AA891276
42	478	77.9	256	23	ABP45734
43	478	77.9	487	22	AB890607
44	478	77.9	487	23	ABG54445
45	477	77.7	118	20	AA806386

ALIGNMENTS

RESULT 1	ABG30446	standard; Protein; 114 AA.
ID	ABG30446	
XX	ABG30446	
AC	ABG30446	
XX	21-OCT-2002	(first entry)
DT	21-OCT-2002	
XX	21-OCT-2002	
DE	Human IGE Fab clone 60 heavy chain protein.	
XX	Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;	
KW	timothy grass pollen allergen; passive immunotherapy.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
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FT		/note= "FR1 region"
FT	Region	27..33
FT		/note= "CDR1 region"
FT	Region	34..47
FT		/note= "FR2 region"
FT	Region	48..63
FT		/note= "CDR2 protein"
FT	Region	64..95
FT		/note= "FR3 region"
FT	Region	96..103
FT		/note= "CDR2 region"
FT	Region	104..114
FT		/note= "FR4 region"
XX		
PN	WO200253595-A1.	

Anti-idiotypic VH
Amyloid peptide co
Amyloid peptide co
Human IgG/factor X
Human HIV-1 monoclonal
Human HIV-1 monoclonal
Human HIV-1 monoclonal
Anti-murine CTLA-4
Humanised LM609 an
Human VEGF-2 relat
The heavy chain of
Human Blys binding
Human Blys binding
Human Blys binding
Human antibody clo
Human Ab heavy cha
Antibody library r
Humanised LM609 an
Amino acid sequenc
Human tKc antibod
Human Blys binding
Human Blys binding
Anti-adipocyte mon
Mab 1-3-1 variable
Human tKc antibod
Variable and first
Human Fab clone LD
ebvHGM MS119D10 h
Anti-TRAIL-R antib
Anti-TRAIL-R antib
Human tKc antibod
Human Blys binding
Human Blys binding
Human secreted pro
Human albumin fusi
Humanised LM609 an

XX 11-JUL-2002.
 PD 27-DEC-2001; 2001WO-SE02908.
 PF 29-DEC-2000; 2000SE-0004892.
 PR (PHMA) PHARMACIA DIAGNOSTICS AB.
 XX
 XX Flicker S, Steindberger P, Kraft D, Valenta R;
 PI
 DR WPI; 2002-583604/62.
 DR N-PSDB; ABK89639.
 XX
 PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for
 PT environmental allergen detection -
 XX
 XX Disclosure; Page 37; 45pp; English.
 PS
 CC This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IgE Fabs and methods for their use. The proteins
 CC of the invention may have anti-allergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's
 CC IgE antibodies to Phi p 2 (a major timothy grass pollen allergen).
 CC The group 2 allergen-specific Fabs of the invention may be useful for
 CC environmental allergen detection and for standardisation of allergen
 CC extracts. The Fabs - or a vaccine against a type I allergy is useful for
 CC passive immunotherapy of type I allergy, it is also useful for
 CC diagnosing a type I allergy. The allergen-specific Fabs of the invention
 CC are useful for inter alia, diagnosis, therapy and prevention of type
 CC I allergy. They are also useful for identification of group 2
 CC allergen-containing pollen and may be used for blocking the binding of
 CC grass pollen allergic patients IgE antibodies to Phi p 2. The present
 CC sequence represents the human IgG fab, clone 60 heavy chain protein of
 CC the invention.
 CC
 CC Sequence 114 AA;
 SO
 Query Match 100.0%; Score 614; DB 23; Length 114;
 Best Local Similarity 100.0%; Pred. No. 4.1e-45;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LESGPELVKPSQTLSTCTVSGSIRSGYYSWVRPCKGLKLEWIGNIYHSGNTYNNPS 60
 DB 1 LESGPELVKPSQTLSTCTVSGSIRSGYYSWVRPCKGLKLEWIGNIYHSGNTYNNPS 60
 QY 61 LKSRITMSVDTSKNHFSLRLTSVTADTAIVYCARSDGYTLDMWOGGLVTYSS 114
 DB 61 LKSRITMSVDTSKNHFSLRLTSVTADTAIVYCARSDGYTLDMWOGGLVTYSS 114
 RESULT 2
 ABG30447 standard; Protein; 114 AA.
 ID ABG30447;
 AC ABG30447;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human IgE Fab clone 100 heavy chain protein.
 XX
 KW Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;
 KM timothy grass pollen allergen; passive immunotherapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..26
 FT /note= "FRI region"
 FT 27..33
 FT /note= "CDR1 region"

FT Region 34..47
 FT /note= "FR2 region"
 FT Region 48..63
 FT /note= "CDR2 protein"
 FT Region 64..95
 FT /note= "FR3 region"
 FT Region 96..103
 FT /note= "CDR2 region"
 FT Region 104..114
 FT /note= "FR4 region"
 XX
 XX WO200253595-A1.
 XX
 PD 11-JUL-2002.
 XX
 XX 27-DEC-2001; 2001WO-SE02908.
 PF
 XX 29-DEC-2000; 2000SE-0004892.
 PR
 XX (PHMA) PHARMACIA DIAGNOSTICS AB.
 PA
 XX Flicker S, Steindberger P, Kraft D, Valenta R;
 PI
 DR WPI; 2002-583604/62.
 DR N-PSDB; ABK89639.
 XX
 PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for
 PT environmental allergen detection -
 XX
 XX Disclosure; Page 38; 45pp; English.
 PS
 CC This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IgE Fabs and methods for their use. The proteins
 CC of the invention may have anti-allergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's
 CC IgE antibodies to Phi p 2 (a major timothy grass pollen allergen).
 CC The group 2 allergen-specific Fabs of the invention may be useful for
 CC environmental allergen detection and for standardisation of allergen
 CC extracts. The Fabs - or a vaccine against a type I allergy is useful for
 CC passive immunotherapy of type I allergy, it is also useful for
 CC diagnosing a type I allergy. The allergen-specific Fabs of the invention
 CC are useful for inter alia, diagnosis, therapy and prevention of type
 CC I allergy. They are also useful for identification of group 2
 CC allergen-containing pollen and may be used for blocking the binding of
 CC grass pollen allergic patients IgE antibodies to Phi p 2. The present
 CC sequence represents the human IgG fab, clone 100 heavy chain protein of
 CC the invention.
 CC
 CC Sequence 114 AA;
 SO
 Query Match 99.0%; Score 608; DB 23; Length 114;
 Best Local Similarity 97.4%; Pred. No. 1.3e-44;
 Matches 111; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LESGPELVKPSQTLSTCTVSGSIRSGYYSWVRPCKGLKLEWIGNIYHSGNTYNNPS 60
 DB 1 LESGPELVKPSQTLSTCTVSGSIRSGYYSWVRPCKGLKLEWIGNIYHSGNTYNNPS 60
 QY 61 LKSRITMSVDTSKNHFSLRLTSVTADTAIVYCARSDGYTLDMWOGGLVTYSS 114
 DB 61 LKSRITMSVDTSKNHFSLRLTSVTADTAIVYCARSDGYTLDMWOGGLVTYSS 114
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 ABG30445 standard; Protein; 114 AA.
 ID ABG30445;
 AC ABG30445;
 XX
 DT 21-OCT-2002 (first entry)
 XX

Human IGE Fab clone 94 heavy chain protein.

KM Human; fab; anti allergic; vaccine; grass pollen; Phi p 2;
KW Timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..26
FT /note= "FR1 region"
FT Region 27..33
FT /note= "CDR1 region"
FT Region 34..47
FT /note= "FR2 region"
FT Region 48..63
FT /note= "CDR2 protein"
FT Region 64..95
FT /note= "FR3 region"
FT Region 96..103
FT /note= "CDR2 region"
FT Region 104..114
FT /note= "FR4 region"

W0200253595-A1.

PN 11-JUL-2002.
PD 27-DEC-2001; 2001WO-SO02908.
PF 29-DEC-2000; 2000SE-0004892.
PR (PHMA) PHARMACIA DIAGNOSTICS AB.
PA
XX Flicker S, Steinberger P, Kraft D, Valenta R;
PI MPI: 2002-583604/62.
DR N-PSDB; ABRK89637.

Group 2 allergen-specific immunoglobulins (Ig) E fabs or IgG comprising variable region of group 2 allergen specific-human IGE fabs, useful for diagnosing or passive immunotherapy of type I allergy, for environmental allergen detection -

Disclosure; Page 36; 45pp; English.

This invention relates to the DNA and protein sequences of group 2 allergen-specific human IGE fabs and methods for their use. The proteins of the invention may have antiallergic activities and may be used as a vaccine or an inhibitor of binding of grass pollen allergic patient's IGE antibodies to Phi p 2 (a major timothy grass pollen allergen). The group 2 allergen-specific fabs of the invention may be useful for environmental allergen detection and for standardisation of allergen extracts. The fabs -or a vaccine against a type I allergy is useful for passive immunotherapy of type I allergy, it is also useful for diagnosing a type I allergy. The allergen-specific fabs of the invention are useful for inter alia, diagnosis, therapy and prevention of type I allergy. They are also useful for identification of group 2 allergen-containing pollen and may be used for blocking the binding of grass pollen allergic patients IGE antibodies to Phi p 2. The present sequence represents the human IGE fab, clone 94 heavy chain protein of the invention.

Sequence 114 AA;

Query Match 88.9%; Score 546; DB 23; Length 114;
Best Local Similarity 89.5%; Pred. No. 2.6e-39;
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0

1 LESGGPLVKKPQTLLELTCTVSGGSIRSGGYVMWPQGKLMEIGNIYHSGNTYNPS 60
|||||||:::||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 LESGGGLVKRPQTLLSLSCANVGSGSIRSOGYTWSWRKHQKGKLEIIGITIHSGNTYNPS 60
|||||||:::||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

61 LKSRTYSVDTSKNHSRLRLTSTVTADTAIVYYCARSDGVETLDNMCGQLTVVSS 114

[illegible]

XX	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; KX
XX	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; KM
XX	common variable immunodeficiency; acquired immunodeficiency syndrome. XX
OS	Homo sapiens.
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XX	WO200202641-A1.
XX	
PD	10-JAN-2002.
XX	
PF	15-JUN-2001; 2001WO-US19110.
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PR	16-JUN-2000; 2000US-212210P.
PR	17-OCT-2000; 2000US-240816P.
PR	16-MAR-2001; 2001US-276248P.
PR	21-MAR-2001; 2001US-277379P.
PR	25-MAY-2001; 2001US-293499P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX	
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX	
DR	WPI; 2002-114799/15.
XX	
PT	Antibodies against B Lymphocyte Stimulating polypeptides, useful for
XX	the diagnosis and treatment of cancers and immune disorders -
XX	
PS	Claim 1; Page 1989-1990; 3148p; English.
XX	
XX	This invention describes novel antibodies that immunospecifically bind to
XX	B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX	tumour necrosis factor (TNF) super family and induces B cell
XX	proliferation and differentiation. The antibodies of the invention have
XX	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX	antirheumatic and antiAIDS activity and can be used in vaccines to
XX	inhibit the expression and activity of Blys. The antibodies bind to Blys
XX	and so may be used to detect and quantitate the presence of Blys in
XX	biological samples and may be used in this way to diagnose disease
XX	associated with aberrant expression of Blys. They may also be
XX	administered to treat diseases associated with aberrant Blys expression
XX	and actively such as cancer, immune, and autoimmune disorders and
XX	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, and
XX	immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX	of the antibodies and fragments of the antibodies described in the method
XX	of the invention.
XX	
SQ	Sequence 252 AA;
XX	
XX	
Query Match	81.6%; Score 501; DB 23; Length 252;
Best Local Similarity	78.5%; Pred. No. 4.1e-35;
Matches 95; Conservative 10; Mismatches 8; Indels 8; Gaps 2	
QY	2 ESGPGLVPSQTLSTLCTVYSGSISGGYYSWMVROPPKSGLEWIGNIYHSGNTYNNPSL 61
DB	6 ESGPGLVPSRSLSLTCTVYSGSISSSSYWGMINQPPKSGLEWIGISITVYSSSTYNNPSL 65
QY	62 KSRITMSVDTSKNHPSLRLTSTYAADTAVYYCARSD----GYTL--DNMGQGLTVYS 113
DB	66 KSRVITISVDTSKNQPSLKLSVYAADTAVYYCARGDYDILTGYPHLAFPIWKGGLTVYS 125
QY	114 S 114
DB	126 S 126
RESULT 8	
AAG80217	
ID	AAG80217 standard; Protein; 127 AA.
AC	AAG80217;
XX	

DT	22-JAN-2002	(first entry)
XX		
DE	Human autoantibody MICA-6 variable region light chain.	
XX		
KW	Autoantigen; fusion protein; islet cell antigen; MICA autoantibody;	
KW	glutamate decarboxylase; diabetes mellitus type I; stiff-man syndrome;	
KW	polyglandular autoimmune syndrome; autoimmune disorder; IA2; GAD65;	
KM	variable region; light chain; MICA-6.	
XX		
OS	Homo sapiens.	
PN	EP1149914-A2.	
XX		
PD	31-OCT-2001.	
XX		
PF	29-MAR-2001; 2001EP-0107702.	
XX		
PR	10-APR-2000; 2000DE-1017782.	
PR	25-MAY-2000; 2000DE-1025840.	
XX		
PA	(LABO-) LABOR KOCH MERK GMBH.	
XX		
PI	Richter W, Rickert M, Rapp I, Dangel W;	
XX		
DR	WPI; 2001-640702/74.	
DR	N-PSDB; AA168766.	
XX		
PT	New fusion protein, useful for diagnosis of diabetes type I and other	
PT	metabolic diseases, is reactive with autoantibodies against both	
PT	glutamate decarboxylase and islet cell antigen	
XX		
PS	Disclosure; Page 35-36; 68pp; German.	
XX		
CC	This invention describes a novel fusion protein (I) that has, at its	
CC	N-terminus, one or more epitopes that bind specifically to autoantibodies	
CC	(Aab) against the islet cell antigen IA2 and, at its C-terminus, one or	
CC	more epitopes that bind specifically to antibodies (Ab) directed against	
CC	the glutamate decarboxylase GAD65. (I), also nucleic acid (II) encoding	
CC	it, vectors containing (II) and transformed cells, are useful for	
CC	diagnosis and prognosis of diabetes mellitus type I, stiff-man syndrome,	
CC	polyglandular autoimmune syndrome or other autoimmune conditions	
CC	associated with Aab against GAD65 or IA2. (I) provides a rapid and simple	
CC	diagnosis of high specificity and sensitivity, capable of recognizing	
CC	antibodies against both IA2 and GAD65, simultaneously. Unlike known	
CC	fusions, where the GAD65 component is at the N-terminus, (I) contains	
CC	correctly folded conformational epitopes that can react with most MICA	
CC	autoantibodies. This sequence represents the human autoantibody MICA-6	
XX	variable region light chain used in the method of the invention.	
XX		
SQ	Sequence 127 AA;	
	Query Match 81.5%; Score 500.5; DB 22; Length 127;	
	Best Local Similarity 78.0%; Pred. No. 2.2e-35;	
	Matches 96; Conservative 7; Mismatches 11; Indels 9; Gaps 1	
QY	1 LESGPGVLKPEPQSTSLTCTVSGSGIRSISGGYMSWVRQPGKGLKLEWIGNIYHSGNTYNYNPS 60	
DB	5 LESGPGVLKPEPSTSLTCTVSGSGISSNNTYMGWIRQPGKGLKLEWISYHSGRTYNYLS 64	
QY	61 LKSRITMSVDTSKNHFSLRLTSTVTAADTAVYYCAR-----DGYTLDNWGQTLVT 111	
DB	65 LKSRITMSVDTSKNQFSLKLTSSVTAADTAVYYCARSYCAVTCYDPDYGLDIMGQITVT 124	
QY	112 VSS 114	
DB	125 VSS 127	
	RESULT 9	
	AAAB30584	
ID	AAAB30584 standard; Protein, 126 AA.	
AC	AAAB30584;	

```

XX
DT 19-MAR-2001 (first entry)
XX
DE A human variable heavy chain region of anti-IgE antibody.
XX
KM Anti-idiotypic antibody; C-epsilon3 region; immunoglobulin E; IgE;
KM anti-IgE antibody; mimobody; vaccine; allergy; asthma; atopic dermatitis;
KM rhinitis; chronic urticaria; food allergy; IgE-mediated disease;
KM passive immunisation.
XX
OS Homo sapiens.
XX
FH Key
FH Region Location/Qualifiers
FT Region 30..37
FT Region /note= "complementarity determining region 1"
FT Region 51..67
FT Region /note= "complementarity determining region 2"
FT Region 100..115
FT Region /note= "complementarity determining region 3"
XX
PN MO200063252-A1.
XX
PD 26-OCT-2000.
XX
PF 12-APR-2000; 2000MO-EP03288.
XX
PR 14-APR-1999; 99GB-0008533.
XX
PA (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PI Kricsek F, Stadler B, Vogel M;
XX
DR WPI; 2000-687161/67.
DR N-PSDB; AAC62336.
XX
PT Novel anti-idiotypic antibody against antibodies which inhibit binding
PT of immunoglobulin E to its high affinity receptor, useful in vaccines
PT for treating diseases such as allergy, rhinitis, atopic dermatitis -
XX
PS Claim 4; Fig 5c; 73pp; English.
XX
CC The present sequence represents a human variable heavy chain region of
CC an anti-idiotypic antibody that interferes with the binding of the
CC C-epsilon3 region of immunoglobulin (Ig)E to the high affinity receptor
CC for IgE, i.e. and anti-IgE antibody. Such an antibody is referred to
CC as a mimobody. The anti-IgE antibody fragment is used as a vaccine, and
CC as a pharmaceutical for treating IgE-mediated diseases such as allergy,
CC in particular asthma, atopic dermatitis, rhinitis, chronic urticaria and
CC food allergies. It is also used to treat IgE-mediated diseases. It is
CC also used for raising polyclonal or monoclonal antibodies. The polyclonal
CC or monoclonal antibodies obtained are useful for treating IgE-mediated
CC diseases by passive immunisation.
XX
SQ Sequence 126 AA;

```

```

Query Match 81.4%; Score 500; DB 21; Length 126;
Best Local Similarity 78.7%; Pred. No. 2.4e-35;
Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

```

```

QY 1 LESGPGLVKPSQTLSTCTVSGGSIIRSGYYWVRPQPKGLEWIGNIYHSGNTYYNPS 60
DB 5 LESGPGLVKPSQTLSTCTVSGGSIIRSGYYWVRPQPKGLEWIGNIYHSGNTYYNPS 64
QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSDG-----YTLDNMGQGTLLTV 112
DB 65 LKSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSDG-----YTLDNMGQGTLLTV 124
QY 113 SS 114
DB 125 SS 126

```

```

RESULT 10
ID ABP54970
ABP54970 standard; Protein; 126 AA.
XX
AC ABP54970;
XX
DT 14-JAN-2003 (first entry)
XX
DE Anti-idiotypic VH sequence mimicking IgE conformational epitope.
XX
KM Human; IgE; immunoglobulin; antibody; epitope; mimotope;
KM lactic acid bacterium; allergy; vaccine; antiallergic;
KM dermatological; antiinflammatory; anti-idiotypic.
XX
OS Homo sapiens.
XX
FH EP1239032-A1.
XX
PD 11-SEP-2002.
XX
PF 02-MAR-2001; 2001EP-0105138.
XX
PR 02-MAR-2001; 2001EP-0105138.
XX
PA (NEST ) SOC PROD NESTLE SA.
XX
PI Stadler BM, Vogel M, Germond J, Fritsche R;
XX
DR WPI; 2002-684058/74.
XX
PT New bacterial strain of lactic acid bacterium group, expressing surface
PT polypeptide which contains peptide sequence mimicking at least part of
PT conformational epitope of immunoglobulin E, useful for treating allergy
XX
PS Claim 4; Page 5; 19pp; English.
XX
CC The present invention relates to recombinant strains of lactic
CC acid bacteria that express surface polypeptides containing
CC peptides (mimotopes) or antibody fragments which mimic at least
CC part of a conformational epitope of an IgE molecule. These are
CC used in food and pharmaceutical compositions, in particular
CC vaccines, for the treatment or prevention of an allergic reaction
CC involving IgE, such as rhinitis, atopic dermatitis and erythema.
CC The mimotope peptides or antibody fragments are obtained by
CC screening random peptide and human Fab antibody phage display
CC libraries with an antibody directed to the Fc part of IgE. The
CC present sequence is the protein sequence of an anti-idiotypic Fab
CC heavy chain variable region (VH) sequence mimicking an IgE
CC conformational epitope.
XX
SQ Sequence 126 AA;

```

```

Query Match 81.4%; Score 500; DB 23; Length 126;
Best Local Similarity 78.7%; Pred. No. 2.4e-35;
Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

```

```

QY 1 LESGPGLVKPSQTLSTCTVSGGSIIRSGYYWVRPQPKGLEWIGNIYHSGNTYYNPS 60
DB 5 LESGPGLVKPSQTLSTCTVSGGSIIRSGYYWVRPQPKGLEWIGNIYHSGNTYYNPS 64
QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSDG-----YTLDNMGQGTLLTV 112
DB 65 LKSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSDG-----YTLDNMGQGTLLTV 124
QY 113 SS 114
DB 125 SS 126

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```

RESULT 11
ID ABG80712
ABG80712 standard; Peptide; 251 AA.

```

XX ABG80712;
 AC 29-NOV-2002 (first entry)
 DT
 XX
 XX Amyloid peptide containing an attachment site #2.
 DE
 XX Molecular antigen array; vaccine; antigen; antimicrobial; mutant;
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza; murein;
 KW graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KW enterokinase; cysteine-containing linker.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200256907-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 21-JAN-2002; 2002WO-IB00168.
 XX
 PR 19-JAN-2001; 2001US-262379P.
 PR 04-MAY-2001; 2001US-288549P.
 PR 05-OCT-2001; 2001US-326998P.
 PR 07-NOV-2001; 2001US-331045P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR/) MAURER P.
 PA (LECH/) LECHNER F.
 PA (ORTM/) ORTMANN R.
 PA (LUEO/) LUEOEND R.
 PA (STAU/) STAUFENBIEL M.
 PA (FREY/) FREY P.
 XX
 PI Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tisot A, Seibel P, Piossek C;
 DR WPI; 2002-636514/68.
 XX
 PT Molecular antigen array used in the production of vaccines for
 PT infectious diseases -
 XX
 PS Claim 38; Page 227; 418pp; English.
 XX
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from:
 CC (1) a core particle of a non-natural origin; and (2) a core particle of
 CC natural origin; and (ii) an organism comprising at least one first
 CC attachment site, where the organism is connected to the core particle by
 CC at least one covalent bond; (b) an antigen or antigenic determinant with
 CC at least one second attachment site, where the antigen or antigenic
 CC determinant is amyloid beta peptide (Abeta 1-42) or its fragment, and
 CC where the second attachment site is selected from: (i) an attachment site
 CC not naturally occurring with the antigen or antigenic determinant; and
 CC (ii) an attachment site naturally occurring with the antigen or
 CC antigenic determinant, where the second attachment site is capable of
 CC association through at least one non-peptide bond to the first attachment
 CC site; and where the antigen or antigenic determinant and the scaffold
 CC interact through the association to form an ordered and repetitive
 CC antigen array. Also included is a process for producing a non-naturally
 CC occurring ordered and repetitive antigen array. The composition is used
 CC in immunisation and as a vaccine for diseases such as influenza,
 CC graft versus host disease, IGE-mediated allergic reactions, anaphylaxis,
 CC adult respiratory distress syndrome (ARDS), Crohn's disease, allergic
 CC asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's

CC disease, systemic lupus erythematosus, inflammatory immune diseases,
 CC myasthenia gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's
 CC disease, osteoporosis and infectious diseases. The present sequence is
 CC a modified antigen for use in the array of the invention. The antigen is
 CC modified to possess a cleavage site (enterokinase or factor Xa) and a
 CC Cysteine-containing N- or C-terminal linker peptide which serves as the
 CC attachment point to a virus like particle or bacterial protein (the
 CC scaffold protein).
 CC
 XX
 SQ Sequence 251 AA;
 XX
 Query Match 81.4%; Score 500; DB 23; Length 251;
 Best Local Similarity 78.7%; Pred. No. 5e-35;
 Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;
 QY 1 LKSGPGLVKSQTLSTCTVSGSIRSGYVSWRPPGKLEWIGNIYHSGNTYVNS 60
 DB 20 LKSGPGLVKSQTLSTCTVSGSIRSGYVSWRPPGKLEWIGNIYHSGNTYVNS 79
 QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYTCARSDG-----YTLDMWGGTTLVTY 112
 DB 80 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYTCARSDG-----YTLDMWGGTTLVTY 139
 QY 113 SS 114
 DB 140 SS 141
 XX
 RESULT 12
 ABG80713
 ID ABG80713 standard; Peptide; 254 AA.
 XX
 XX ABG80713;
 XX
 DT 29-NOV-2002 (first entry)
 DT
 XX
 XX Amyloid peptide containing an attachment site #3.
 DE
 XX Molecular antigen array; vaccine; antigen; antimicrobial; mutant;
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza; murein;
 KW graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KW enterokinase; cysteine-containing linker.
 KW
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200256907-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 21-JAN-2002; 2002WO-IB00168.
 XX
 PR 19-JAN-2001; 2001US-262379P.
 PR 04-MAY-2001; 2001US-288549P.
 PR 05-OCT-2001; 2001US-326998P.
 PR 07-NOV-2001; 2001US-331045P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR/) MAURER P.
 PA (LECH/) LECHNER F.
 PA (ORTM/) ORTMANN R.
 PA (LUEO/) LUEOEND R.
 PA (STAU/) STAUFENBIEL M.

PA (FRET/) FREY P.
 XX Maurer P, Lechner F, Ottmann R, Luecend R, Staufenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tiesot A, Sebbel P, Piossek C;
 XX WPI; 2002-636514/68.
 DR
 XX Molecular antigen array used in the production of vaccines for
 PT infectious diseases -
 PS Claim 38; Page 227; 418pp; English.
 XX
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from:
 CC (1) a core particle of a non-natural origin; and (2) a core particle of
 CC natural origin; and (ii) an antigen or antigenic determinant with
 CC attachment site, where the antigen is connected to the core particle by
 CC at least one covalent bond; (b) an antigen or antigenic determinant with
 CC at least one second attachment site, where the antigen or antigenic
 CC determinant is amyloid beta peptide (Abeta 1-42) or its fragment, and
 CC where the second attachment site is selected from: (i) an attachment site
 CC not naturally occurring with the antigen or antigenic determinant; and
 CC (ii) an attachment site naturally occurring with the antigen or
 CC antigenic determinant, where the second attachment site is capable of
 CC association through at least one non-peptide bond to the first attachment
 CC site; and where the antigen or antigenic determinant and the scaffold
 CC interact through the association to form an ordered and repetitive
 CC antigen array. Also included is a process for producing a non-naturally
 CC occurring ordered and repetitive antigen array. The composition is used
 CC in immunisation and as a vaccine for diseases such as influenza,
 CC graft versus host disease, IGE-mediated allergic reactions, anaphylaxis,
 CC adult respiratory distress syndrome (ARDS), Crohn's disease, allergic
 CC asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's
 CC disease, systemic lupus erythematosus, inflammatory immune diseases,
 CC myasthenia gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's
 CC disease, osteoporosis and infectious diseases. The present sequence is
 CC a modified antigen for use in the array of the invention. The antigen is
 CC modified to possess a cleavage site (enterokinase or factor Xa) and a
 CC cysteine-containing N- or C-terminal linker peptide which serves as the
 CC attachment point to a virus like particle or bacterial protein (the
 CC scaffold protein).
 XX
 XX Sequence 254 AA;
 SQ
 Query Match 81.4%; Score 500; DB 23; Length 254;
 Best local Similarity 78.7%; Pred. No. 5e-35;
 Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;
 QY 1 LBSGPGILVPSQTLSTLTCTVSGSIRSGYVWVROPKGLFIGNITHSNTYVNP 60
 DB 20 LBSGPGILVPSQTLSTLTCTVSGSIRSGYVWVROPKGLFIGNITHSNTYVNP 79
 QY 61 LKSRITVSVTSKQHFSLRLTSVTAADTAVYVYCARSG-----YTLNMGQGLTVV 112
 DB 80 LKSRITVSVTSKQHFSLRLTSVTAADTAVYVYCARSG-----YTLNMGQGLTVV 139
 QY 113 SS 114
 DB 140 SS 141
 RESULT 13
 ABG80714
 ID ABG80714 standard; Protein; 263 AA.
 XX
 AC ABG80714;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 DE Human IgG/factor Xa cleavage site fusion protein from pCep--Xa-Fc*.

KW Molecular antigen array; vaccine; antigen; antimicrobial; mutant;
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza; mutagen;
 KW graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KW enterokinase; cysteine-containing linker.
 XX
 OS Homo sapiens.
 OS Synthetic.
 EN WO200256907-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 21-JAN-2002; 2002WO-1B00168.
 XX
 PR 19-JAN-2001; 2001US-262379P.
 PR 04-MAY-2001; 2001US-288549P.
 PR 05-OCT-2001; 2001US-326998P.
 PR 07-NOV-2001; 2001US-331045P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PI (MAUR/) MAURER P.
 PI (LECH/) LECHNER F.
 PA (ORTM/) ORTMANN R.
 PA (LUEC/) LUECEND R.
 PA (STAU/) STAUFENBIEL M.
 PA (FRET/) FREY P.
 XX
 XX Maurer P, Lechner F, Ottmann R, Luecend R, Staufenbiel M, Frey P;
 PI Renner WA, Bachmann M, Tiesot A, Sebbel P, Piossek C;
 XX WPI; 2002-636514/68.
 DR N-PSDB; ABS66508.
 DR
 PT Molecular antigen array used in the production of vaccines for
 PT infectious diseases -
 XX
 PS Example 1; Fig 1; 418pp; English.
 XX
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from:
 CC (1) a core particle of a non-natural origin; and (2) a core particle of
 CC natural origin; and (ii) an antigen or antigenic determinant with
 CC attachment site, where the antigen is connected to the core particle by
 CC at least one covalent bond; (b) an antigen or antigenic determinant with
 CC at least one second attachment site, where the antigen or antigenic
 CC determinant is amyloid beta peptide (Abeta 1-42) or its fragment, and
 CC where the second attachment site is selected from: (i) an attachment site
 CC not naturally occurring with the antigen or antigenic determinant; and
 CC (ii) an attachment site naturally occurring with the antigen or
 CC antigenic determinant, where the second attachment site is capable of
 CC association through at least one non-peptide bond to the first attachment
 CC site; and where the antigen or antigenic determinant and the scaffold
 CC interact through the association to form an ordered and repetitive
 CC antigen array. Also included is a process for producing a non-naturally
 CC occurring ordered and repetitive antigen array. The composition is used
 CC in immunisation and as a vaccine for diseases such as influenza,
 CC graft versus host disease, IGE-mediated allergic reactions, anaphylaxis,
 CC adult respiratory distress syndrome (ARDS), Crohn's disease, allergic
 CC asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's
 CC disease, systemic lupus erythematosus, inflammatory immune diseases,
 CC myasthenia gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's
 CC disease, osteoporosis and infectious diseases. The present sequence is
 CC a modified antigen for use in the array of the invention. The antigen is

modified to possess a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N- or C-terminal linker peptide which serves as the attachment point to a virus like particle or bacterial protein (the scaffold protein).

Sequence 263 AA;

Query Match 81.4%; Score 500; DB 23; Length 263;

Best Local Similarity 78.7%; Pred. No. 5.2e-35;

Matches 96; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWVWVOPFGKLEWIGNIYHSGNTYVNS 60
DB 20 LESGPGLVKPSQTLSTCTVSGSIRSGGYWVWVOPFGKLEWIGNIYHSGNTYVNS 79
DY 61 LKSRITMSVDTSKNHPSRLTSVTAADTAAYVVCARSDG-----YTLDMNGGTLVTV 112
DB 80 LKSRITMSVDTSKNHPSRLTSVTAADTAAYVVCARSDG-----YTLDMNGGTLVTV 139
QY 113 SS 114
DB 140 SS 141

RESULT 14

AAB62775 ID AAB62775 standard; Protein, 120 AA.

AC AAB62775;

DT 03-APR-2001 (first entry)

DE Human HIV-1 monoclonal antibody SEQ ID NO: 74.

XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;

KW envelope glycoprotein; gp120; diagnosis.

OS Homo sapiens.

PN WO200100678-A1.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-US17327.

PR 30-JUN-1999; 99US-0141701.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Watkins BA, Reitz MS;

DR WPI; 2001-112438/12.

DR N-PSDB; AAF29076.

PT Novel human monoclonal antibody immunoreactive with human

PT immunodeficiency virus-1 glycoprotein gp120; useful for detecting HIV-1

PT in biological sample and providing passive immunotherapy to HIV-1

PT infected mammal

PS Claim 1; Page 69; 81pp; English.

XX The present invention provides the protein and coding sequences for the

CC variable regions of human monoclonal antibodies which are immunoreactive

CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.

CC These can be used in diagnosis and therapy of HIV-1 infection.

DB 7 ESGGGLVPSQTLSTCTVSGSIRSGGYWVWVOPFGKLEWIGNIYHSGNTYVNSL 66
QY 62 KSRITMSVDTSKNHPSRLTSVTAADTAAYVVCARSDG-----YTLDMNGGTLVTVSS 114
DB 67 KSRITMSVDTSKNHPSRLTSVTAADTAAYVVCARSDG-----YTLDMNGGTLVTVSS 120

RESULT 15

AAB62745 ID AAB62745 standard; Protein, 123 AA.

AC AAB62745;

DT 03-APR-2001 (first entry)

DE Human HIV-1 monoclonal antibody SEQ ID NO: 44.

XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;

KW envelope glycoprotein; gp120; diagnosis.

OS Homo sapiens.

PN WO200100678-A1.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-US17327.

PR 30-JUN-1999; 99US-0141701.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Watkins BA, Reitz MS;

DR WPI; 2001-112438/12.

DR N-PSDB; AAF29046.

PT Novel human monoclonal antibody immunoreactive with human

PT immunodeficiency virus-1 glycoprotein gp120; useful for detecting HIV-1

PT in biological sample and providing passive immunotherapy to HIV-1

PT infected mammal

PS Claim 1; Page 50; 81pp; English.

XX The present invention provides the protein and coding sequences for the

CC variable regions of human monoclonal antibodies which are immunoreactive

CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.

CC These can be used in diagnosis and therapy of HIV-1 infection.

XX Sequence 123 AA;

Query Match 81.4%; Score 498; DB 22; Length 123;

Best Local Similarity 80.3%; Pred. No. 3.5e-35;

Matches 94; Conservative 10; Mismatches 9; Indels 4; Gaps 1;

QY 2 ESGGGLVPSQTLSTCTVSGSIRSGGYWVWVOPFGKLEWIGNIYHSGNTYVNSL 61

DB 7 ESGGGLVPSQTLSTCTVSGSIRSGGYWVWVOPFGKLEWIGNIYHSGNTYVNSL 66

QY 62 KSRITMSVDTSKNHPSRLTSVTAADTAAYVVCARSDG-----YTLDMNGGTLVTVSS 114

DB 67 KSRITMSVDTSKNHPSRLTSVTAADTAAYVVCARSDG-----YTLDMNGGTLVTVSS 123

Search completed: February 10, 2004, 18:36:09

Job time : 35.3727 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:39:30 ; Search time 26.2545 Seconds

(without alignments)
909.160 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614

Sequence: 1 LESGRLVKSQTLSTFCTV.....RSDGYTLDNWGQTLVTSS 114

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	614	100.0	114	US-10-027-725A-8	Sequence 8, Appli
2	600	97.7	114	US-10-027-725A-9	Sequence 9, Appli
3	546	88.9	114	US-10-027-725A-7	Sequence 7, Appli
4	510.5	83.1	121	US-10-309-762-152	Sequence 152, App
5	510	83.1	118	US-10-309-762-138	Sequence 138, App
6	509.5	82.0	123	US-10-309-762-10	Sequence 10, Appl
7	507.5	82.7	125	US-10-309-762-11	Sequence 11, Appl
8	507	82.6	120	US-10-309-762-13	Sequence 13, Appl
9	507	82.6	120	US-10-309-762-144	Sequence 144, App
10	507	82.6	122	US-10-309-762-147	Sequence 147, App
11	506	82.4	121	US-09-972-656-80	Sequence 80, Appl
12	505.5	82.3	121	US-10-309-762-151	Sequence 151, App
13	504.5	82.2	117	US-10-330-613-13	Sequence 13, Appl
14	504.5	82.2	117	US-10-330-613-13	Sequence 13, Appl
15	503.5	82.0	119	US-10-309-762-140	Sequence 140, App

16	502.5	81.8	123	US-10-309-762-12	Sequence 12, Appl
17	502	81.8	124	US-10-309-762-75	Sequence 75, Appl
18	502	81.8	143	US-10-309-762-96	Sequence 96, Appl
19	501	81.6	252	US-09-880-748-1329	Sequence 1329, Ap
20	500	81.4	120	US-10-309-762-128	Sequence 128, App
21	500	81.4	120	US-10-309-762-139	Sequence 139, App
22	500	81.4	121	US-10-308-817-137	Sequence 137, App
23	500	81.4	126	US-09-974-449-6	Sequence 6, Appli
24	499	81.3	116	US-10-309-762-127	Sequence 127, App
25	498.5	81.2	125	US-10-309-762-8	Sequence 8, Appli
26	498.5	81.2	125	US-10-309-762-16	Sequence 16, Appl
27	497.5	81.0	119	US-10-309-762-131	Sequence 131, App
28	497	80.9	110	US-10-309-762-74	Sequence 74, Appl
29	496.5	80.9	123	US-10-309-762-9	Sequence 9, Appli
30	496.5	80.9	127	US-10-309-762-14	Sequence 14, Appl
31	495.5	80.7	113	US-10-309-762-148	Sequence 148, App
32	495	80.6	118	US-10-078-7578-52	Sequence 52, Appl
33	494.5	80.5	125	US-10-309-762-153	Sequence 153, App
34	494.5	80.5	251	US-10-120-414-75	Sequence 75, Appl
35	494	80.5	172	US-10-153-382-21	Sequence 21, Appl
36	493.5	80.4	117	US-10-330-613-5	Sequence 5, Appli
37	493.5	80.4	117	US-10-330-530-5	Sequence 5, Appli
38	493.5	80.4	123	US-10-309-762-17	Sequence 17, Appl
39	493	80.3	252	US-09-880-748-1994	Sequence 1994, Ap
40	492.5	80.2	119	US-10-309-762-143	Sequence 143, App
41	492.5	80.2	251	US-09-880-748-990	Sequence 990, App
42	492.5	80.2	253	US-09-880-748-1619	Sequence 1619, Ap
43	491.5	80.0	117	US-10-309-762-22	Sequence 22, Appl
44	491.5	80.0	123	US-10-309-762-18	Sequence 18, Appl
45	491.5	80.0	123	US-10-309-762-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-10-027-725A-8

Sequence 8, Application US/10027725A

Publication No. US20030082659A1

GENERAL INFORMATION:

APPLICANT: Flicker, Sabine

TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use thereof

FILE REFERENCE: 25401-4

CURRENT FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US/10/027,725A

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SEQ ID NO 8

LENGTH: 114

TYPE: PRT

ORGANISM: Homo sapiens

US-10-027-725A-8

Query Match 100.0%; Score 614; DB 15; Length 114;

Best Local Similarity 100.0%; Pred. No. 2.5e-49;

Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESGRLVKSQTLSTFCTVSGSIRSGGYWVWVOPPGKLEWIGNIYHSGTYNPS 60

DB 1 LESGRLVKSQTLSTFCTVSGSIRSGGYWVWVOPPGKLEWIGNIYHSGTYNPS 60

QY 61 LKSRITVSDTSKXHFSLRTSVTAADTAVYYCARSDGYTLDNWGQTLVTSS 114

DB 61 LKSRITVSDTSKXHFSLRTSVTAADTAVYYCARSDGYTLDNWGQTLVTSS 114

RESULT 2

US-10-027-725A-9

Sequence 9, Application US/10027725A

Publication No. US20030082659A1

GENERAL INFORMATION:

/ APPLICANT: Flicker, Sabine
 / TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
 / FILE REFERENCE: 25401-4
 / CURRENT APPLICATION NUMBER: US/10/027,725A
 / CURRENT FILING DATE: 2002-08-09
 / PRIOR APPLICATION NUMBER: US 607,259,436
 / PRIOR FILING DATE: 2000-12-29
 / NUMBER OF SEQ ID NOS: 12
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 9
 / LENGTH: 114
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / US-10-027-725A-9

Query Match 97.7%; Score 600; DB 15; length 114;
Best Local Similarity 96.5%; Pred. No. 4.8e-48;
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LESGPGELVPSQTLSLTCTVSGGSIKSGGYMSWNRQPPGKGLEWIGNITHSGNTYNPSS 600

DB 1 LESGPGELVPSQTLSLTCTVSGGSIKSGGYMSWNRQPPGKGLEWIGIYHSGNTYNPSS 600

```

Qy      61 LKSRITMSVDTSKNHFSRLRTSYAADTAIVYYCARSDGYTLDMNGGGLTVTSS 114
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 LKSRVTMSVDTSKNHFSRLRSTSYAADTAIVYYCARSDGYTLDMNGGGLTVTSS 114

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RESULT 3
US-10-027-725A-7
; Sequence 7, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIORITY FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-725A-7

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Query Match	88.9%	Score 546	DB 15	Length 114
Beet Local Similarity	89.5%	Pred. No. 4.6e-43		
Matches 102	Conservative 4	Mismatches 8	Indels 0	Gaps 0
Oy	1	LESGPGLVKPQSLTSLCTVSGSGSIRSGGYWMSVROPDGGKLEWIGNINHSGMTYNP	60	
		: : : : : : : : : :		
		: : : : : : : : :		
Db	1	LESGGLVKPAQTLTSLSCAVSGGSIIRSGGYWMSIRHPGKGLWIGIYHSGMTYNP	60	
Oy	61	LKSRITMSVDPDKHPSLRLTSYTAADTAAYVYCARSDGYTLDDNNGGTLTVSS	114	
		: : : : : : : : :		
Db	61	LKSIITMSVDPSEKPSLRLTMSVTAADTAAYVYCARLDGYTLDDNNGGTLTVSS	114	

RESULT 4
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018196A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michel
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE INHIBITORS
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A

```

:
: CURRENT APPLICATION NUMBER: US/10/309,762
:
: CURRENT FILING DATE: 2002-12-02
:
: PRIOR APPLICATION NUMBER: 60/337275
:
: PRIOR FILING DATE: 2001-12-03
:
: NUMBER OF SEQ ID NOS: 246
:
: SOFTWARE: FASTSQ for Windows Version 4.0
:
: SEQ ID NO 152
:
: LENGTH: 121
:
: TYPE: prt
:
: ORGANISM: Homo sapiens
:
: US-10-309-762-152

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Query Match	83.1%	Score	510.5	DB	12	Length	121
Best Local Similarity	82.8%	Pred. No.	9	2e-40			
Matches	96	Conservative	8	Mismatches	9	Indels	3
						Gaps	1

```
OY      2 ESGPGLVKPSQTLSTCTVSGSIRSGCYWMSVRPPGKGLEIGNIYHSNGTYNPSL 61
        |||||
Db       6 ESGPGLVKPSQTLSTCTVSGSISGCGYWMSIRQHPKGLEIGNIYYSGSTYNPSL 65
```

```
QY      62 KSRIMSVDTSKNHFLRLTSTVAADTAHYCCARD--GYTLDNNGOGLTVTVSS    114
        |||::||| |||::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      66 KSRVTSVDTSKQFSLKLTSSVTAAADTAHYCAYYDILTGAFDIWGGTMVTVSS    121
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```

RESULT 5
US-10-309-762-138
: Sequence 138, Application US/10309762
: Publication No. US20040018158A1
: GENERAL INFORMATION:
: APPLICANT: Gudas, Jean
: APPLICANT: Foltz, Ian
: APPLICANT: Handa, Masahisa
: APPLICANT: Gallo, Michael
: TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE
: TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
: FILE REFERENCE: ABGENIX 027A
: CURRENT APPLICATION NUMBER: US/10/309,762
: CURRENT FILING DATE: 2002-12-02
: PRIOR APPLICATION NUMBER: 60/337275
: PRIOR FILING DATE: 2001-12-03
: NUMBER OF SEQ ID NOS: 246
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 138
: LENGTH: 118
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-309-762-138

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	Query Match	83.1%	Score 510;	DB 12,	Length 118;
	Best Local Similarity	85.0%;	Pred. No.	1e-39;	Mismatches 7; Indels 0; Gaps 0
	Matches	96;	Conservative	10;	
Oy	2 ESGBPVLVSPQTLLSTCTCGSGSIRGGGYMSWROPBGKLEWIGNITYHSGNTYNSPL		:	: :	61
Dd	6 ESGGGLVPSSQTLTLCVSCGSISGGYSWSMRHPKGLEWIGYYISSGTYNPSL		:	: :	65
Oy	62 KSRITMSVDTSKNFSLRLTVTAADTYVVYCARSDDGYTLDNMGOGTLVTSS		:	: :	114
Dd	66 KSRYATISDVDSIKNPSSLKLSSVTADAIVVCARYGSGSDIMWGOGTLVTSS		:	: :	118

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RESULT 6
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US2004001819A1
; GENERAL INFORMATION:
; APPLICANT: Gudea, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IN
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

```

RESULT 10
US-10-309-762-147
: Sequence 147, Application US/10309762
: Publication No. US20040018198A1
: GENERAL INFORMATION:
: APPLICANT: Gudas, Jean
: APPLICANT: Foltz, Ian
: APPLICANT: Hadda, Maahiba
: APPLICANT: Gallo, Michael

RESULT 12
US-10-309-762-151
Sequence 151, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE INHIBITORS
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX-027A

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, RESULT 14
, US-10-330-530-13
, Sequence 13, Application US/10330530
, Publication No. US2003015251A1
, GENERAL INFORMATION:
, APPLICANT: Gudas, Jean
, TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
, RILE REFERENCE: AGENTX 031A
, CURRENT APPLICATION NUMBER: US/10/330,530
, CURRENT FILING DATE: 2002-12-26
, PRIOR APPLICATION NUMBER: US 60/346414
, PRIOR FILING DATE: 2001-12-18
, NUMBER OF SEQ. ID NOS: 40
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 13

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Human immune system
Human BLYS binding
The heavy chain of
Human HV-1 monoclonal
Human tritc antibody
A human variable h
Anti-idiotypic VH
Human tritc antibody
Amyloid peptide cc
Amyloid peptide cc
Human IgG/factor x
Humanised LM609 a
Humanised LM609 a
Human tritc antibody
Human BLYS binding
Human secreted protein
Human albumin fusion
Anti-murine CTLA-4
Humanised LM609 a
Humanised LM609 a
Human BLYS binding
Human BLYS binding
Variable and first
Mab GAH variable 1
Human Ab heavy chain
Human GAH antibody
Human GAH antibody
Anti-body library
Human BLYS binding
Human autotantibody
Human anti-SP1B/1d
Human antibody cld
Human BLYS binding
Human BLYS binding
Anti-adipocyte monoclonal
Humanised LM609 a
Human immunoglobulin

```

XX 11-JUL-2002.
PD 27-DEC-2001; 2001WO-SE02908.
PF 29-DEC-2000; 2000SE-0004892.
XX (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX Flicker S, Steinberger P, Kraft D, Valenta R;
XX WPI; 2002-583604/62.
XX N-PSDB; ABK89637.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for
XX environmental allergen detection -
XX
XX Disclosure; Page 36; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's
CC IgE antibodies to Phi p 2 (a major timothy grass pollen allergen).
CC The group 2 allergen-specific Fabs of the invention may be useful for
CC environmental allergen detection and for standardisation of allergen
CC extracts. The Fabs - or a vaccine against a type I allergy is useful for
CC passive immunotherapy of type I allergy, it is also useful for
CC diagnosing a type I allergy. The allergen-specific Fabs of the invention
CC are useful for inter alia, diagnosis, therapy and prevention of type
CC I allergy. They are also useful for identification of group 2
CC allergen-containing pollen and may be used for blocking the binding of
CC grass pollen allergic patients IgE antibodies to Phi p 2. The present
CC sequence represents the human IgG fab, clone 94 heavy chain protein of
CC the invention.
XX
XX Sequence 114 AA;
SQ
Query Match 100.0%; Score 609; DB 23; Length 114;
Best Local Similarity 100.0%; Pred. No. 4,8e-50;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LESGPGLVKPAQTLISLSCAVSGSIRSGYVSMIRHPGKGLMWIGYIYHSGNTYVNS 60
DB 1 LESGPGLVKPAQTLISLSCAVSGSIRSGYVSMIRHPGKGLMWIGYIYHSGNTYVNS 60
QY 61 LKSRIMSVDTSENKFSRLNSVTAAADTAVVYCARLDGYTLDIWGGTLVTVSS 114
DB 61 LKSRIMSVDTSENKFSRLNSVTAAADTAVVYCARLDGYTLDIWGGTLVTVSS 114
RESULT 2
ABG30447 standard; Protein: 114 AA.
XX
XX ABG30447;
AC
XX
XX 21-OCT-2002 (first entry)
DT
XX
XX Human IgE Fab clone 100 heavy chain protein.
DE
XX
XX Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
XX timothy grass pollen allergen; passive immunotherapy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..26
FT Region /note= "FR1 region"
FT 27..33
FT Region /note= "CDR1 region"

```

```

FT Region 34..47
FT /note= "FR2 region"
FT Region 48..63
FT /note= "CDR2 protein"
FT Region 64..95
FT /note= "FR3 region"
FT Region 96..103
FT /note= "CDR2 region"
FT Region 104..114
FT /note= "FR4 region"
XX
XX WO200253595-A1.
XX
XX 11-JUL-2002.
PD
XX
XX 27-DEC-2001; 2001WO-SE02908.
PF
XX
XX 29-DEC-2000; 2000SE-0004892.
PR
XX
XX (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX
XX Flicker S, Steinberger P, Kraft D, Valenta R;
XX WPI; 2002-583604/62.
XX N-PSDB; ABK89639.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for
XX environmental allergen detection -
XX
XX Disclosure; Page 38; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's
CC IgE antibodies to Phi p 2 (a major timothy grass pollen allergen).
CC The group 2 allergen-specific Fabs of the invention may be useful for
CC environmental allergen detection and for standardisation of allergen
CC extracts. The Fabs - or a vaccine against a type I allergy is useful for
CC passive immunotherapy of type I allergy, it is also useful for
CC diagnosing a type I allergy. The allergen-specific Fabs of the invention
CC are useful for inter alia, diagnosis, therapy and prevention of type
CC I allergy. They are also useful for identification of group 2
CC allergen-containing pollen and may be used for blocking the binding of
CC grass pollen allergic patients IgE antibodies to Phi p 2. The present
CC sequence represents the human IgG fab, clone 100 heavy chain protein of
CC the invention.
XX
XX Sequence 114 AA;
SQ
Query Match 89.8%; Score 547; DB 23; Length 114;
Best Local Similarity 89.5%; Pred. No. 3,4e-44;
Matches 102; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 LESGPGLVKPAQTLISLSCAVSGSIRSGYVSMIRHPGKGLMWIGYIYHSGNTYVNS 60
DB 1 LESGPGLVKPAQTLISLSCAVSGSIRSGYVSMIRHPGKGLMWIGYIYHSGNTYVNS 60
QY 61 LKSRIMSVDTSENKFSRLNSVTAAADTAVVYCARLDGYTLDIWGGTLVTVSS 114
DB 61 LKSRIMSVDTSENKFSRLNSVTAAADTAVVYCARLDGYTLDIWGGTLVTVSS 114
RESULT 3
ABG30446 standard; Protein: 114 AA.
XX
XX ABG30446;
AC
XX
XX 21-OCT-2002 (first entry)
DT
XX

```

Human IgE Fab clone 60 heavy chain protein.

Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;
timothy grass pollen allergen; passive immunotherapy.

Homo sapiens.

Key	Location/Qualifiers
FT Region	1..26 /note= "FR1 region"
FT Region	27..33 /note= "CDR1 region"
FT Region	34..47 /note= "FR2 region"
FT Region	48..63 /note= "CDR2 protein"
FT Region	64..95 /note= "FR3 region"
FT Region	96..103 /note= "CDR2 region"
FT Region	104..114 /note= "FR4 region"

WO200253595-A1.

11-JUL-2002.

27-DEC-2001; 2001WO-S02908.

29-DEC-2000; 2000SE-0004892.

(PHAA) PHARMACIA DIAGNOSTICS AB.

Flicker S, Steinberger P, Kraft D, Valenta R;
MPI: 2002-583604/62.
N-PSTDB; ABR89638.

Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising variable region of group 2 allergen specific-human IgE Fabs, useful for diagnosing or passive immunotherapy of type I allergy, for environmental allergen detection -

Disclosure; Page 37; 45pp; English.

This invention relates to the DNA and protein sequences of group 2 allergen-specific human IgE Fabs and methods for their use. The proteins of the invention may have anti-allergic activities and may be used as a vaccine or an inhibitor of binding of grass pollen allergic patient's IgE antibodies to Phi p 2 (a major timothy grass pollen allergen). The group 2 allergen-specific fabs of the invention may be useful for environmental allergen detection and for standardisation of allergen extracts. The fabs - or a vaccine against a type I allergy is useful for passive immunotherapy of type I allergy, it is also useful for diagnosing a type I allergy. The allergen-specific fabs of the invention are useful for inter alia, diagnosis, therapy and prevention of type I allergy. They are also useful for identification of group 2 allergen-containing pollen and may be used for blocking the binding of grass pollen allergic patients IgE antibodies to Phi p 2. The present sequence represents the human IgE fab, clone 60 heavy chain protein of the invention.

Sequence 114 AA;

```

Query Match      89.7%; Score 546; DB 23; Length 114;
Best Local Similarity 89.5%; Pred. No. 4, 2e-44;
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0
1 LESGGGLVKPQQTSLSCAVSGGSIRSGGYWVSWIRHPHGKGLNIYGIYHSGNTYNPS 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
1 LESGGGLVKPQQTSLSLCTVSGGSIIRSGGYWVSWIRHPHGKGLNIYHSGNTYNPS 60
61 LKSRIAMSVDTSENKFSRLNLSVTADVAIVYYCARLDGVTLTDIMWGQLTVLVSS 114

```

Db 61 LKSRITWSVPTSKNHFSRLTSTVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114

RESULT 4
 ID AAW78433
 AAW78433 standard; Protein; 123 AA.
 AC AAW78433;
 DT 11-MAY-1999 (first entry)
 XX Antibody heavy chain targeted to obr clone 26.
 DE
 KM Variant; antibody; heavy chain; light chain; immunoadhesin; immunoassay;
 KW diagnosis; cancer; primer; PCR; amplification; dicistronic.
 XX
 OS Synthetic.
 NC WO9850431-A2.
 PN 12-NOV-1998.
 PD
 XX 30-APR-1998; 98WO-US08762.
 XX 24-JUN-1997; 97US-0050661.
 PR 02-MAY-1997; 97US-0850058.
 PA (GETH) GENENTECH INC.
 XX
 XX Arethoon R, Carter PJ, Merchant AM, Presta LG;
 PI WPI; 1999-070091/06.
 DR
 XX
 XX Selective preparation of multispecific antibodies - with
 PT heteromultimeric heavy chain and common light chain components,
 PT useful for, e.g. in vivo diagnosis of cancer
 XX
 XX Example 4; Fig 5; 69pp; English.

This sequence represents the heavy chain variable region for an antibody that binds to the obr clone 26 protein. The sequence encoding the chain is generated by a new method for preparing a multispecific Ab comprising a first polypeptide (PP) and at least 1 extra PP, where: (i) the first PP comprises a multimerisation domain (MD) forming an interface positioned to interact with an interface of a MD of the extra PP; and (ii) the first and extra PPs each have a binding domain, which comprises a heavy chain and a light chain, where the variable light chains of the first and extra PPs comprise a common sequence. The method comprises: (a) culturing a host cell comprising nucleic acid encoding the first PP and extra PP, and the variable light chain, such that the nucleic acid is expressed; and (b) recovering the multispecific Ab from the culture. The method prepares heteromultimeric PPs, such as bispecific Abs, bispecific immunoadhesins and Ab-immunoadhesin chimeras. The method allows for the enhanced formation of the desired heteromultimer relative to the undesired heteromultimers and homomultimers. The Abs can be used in immunoassays and for the in vitro or in vivo diagnosis of various diseases, such as cancer.

Sequence 123 AA;
 SQ

Query Match 83.2%; Score 506.5; DB 20; Length 123;
 Best Local Similarity 79.0%; Pred. No. 2,56-40;
 Matches 94; Conservative 12; Mismatches 8; Indels 5; Gaps 1;

1 LESGPGILVKPAQTLISLCAVSGGSIIRSGYIWSIRHPKGLFWIGIYHSGNTYTPS 60
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 5 VESGPGILVKPSQTLISLCTVSGGSIIRSGYIWSIRHPKGLFWIGIYHSGNTYTPS 64
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 61 LKSRITWSVPTSKNHFSRLTSTVTAADTAVYYCARL-----GYTLDMWGQGLTVTVSS 114
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 65 LKSRITWSVPTSKNHFSRLTSTVTAADTAVYYCARLVDLEIDYGASADPWGGGLTVTVSS 123
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5

ID ABB97976 standard; Protein; 123 AA.

XX ABB97976;

DT 06-SEP-2002 (first entry)

XX Heavy chain variable region from antibody obr.26.

XX Antibody; bispecific antibody; immunoadhesin; cytostatic; antibacterial;
KM antiviral; vaccine; tumour.

XX Synthetic.

PN US2002062010-A1.

PD 23-MAY-2002.

PF 23-MAY-2001; 2001US-0863693.

PR 02-MAY-1997; 97US-046816P.

PR 30-APR-1998; 98US-0070166.

PA (GETH) GENENTECH INC.

PI Arathoon WR, Carter PJ, Merchant AM, Presta LG;

DR MPI; 2002-499676/53.

XX New multispecific antibodies having heteromultimeric and common
PT components are useful to direct treatment to a target site such as a
PT tumour cell, cell surface receptor or clon, as a vaccine adjuvant and to
PT treat infectious disease

PS Example 4; Fig 5; 36pp; English.

XX The invention relates to a new multispecific antibody, comprising at
CC least two polypeptides (PP1 and PP2) which meet at a multiface, where PP1
CC has a multimerisation domain forming an interface positioned to interact
CC with an interface of a multimerisation domain of PP2, and both
CC polypeptides each comprise a binding domain consisting a heavy chain and
CC a variable light chain, where the light chain has a sequence common to
CC both polypeptides. Heteromultimers of the invention include bispecific
CC antibodies, bispecific immunoadhesins and antibody-immunoadhesin
CC chimeras. The activity of antibodies of the invention may be described
CC as, cytostatic, antibacterial and antiviral. The heteromultimer
CC can be used for redirected cytotoxicity, for example to kill tumour
CC cells, as a vaccine adjuvant, for delivering thrombolytic agents to
CC clots, for converting enzyme activated prodrugs at a target site such as
CC a tumour, for treating infectious diseases, for targeting immune
CC complexes to cell surface receptors or for delivering immunotoxins to
CC tumour cells. The current sequence represents the heavy chain variable
CC region from antibody obr.26 used in the construction of bispecific
CC antibodies.

XX Sequence 123 AA;

SQ Query Match 83.2%; Score 506.5; DB 23; Length 123;

Best Local Similarity 79.0%; Pred. No. 2.5e-40;

Matches 94; Conservative 12; Mismatches 8; Indels 5; Gaps 1;

QY 1 LESGPGIVKPAQTLISCAVSGSIRSGYWMIRHPEKGLEWIGYIYHSQNTYNNPS 60

DB 5 VESGPGIVKPSQTLISLTCTVSGSISGSGYWMIRHPEKGLEWIGYIYSSSTYNNPS 64

QY 61 LKSRIMSVDTSENKPSLRINSVTAAADTAVYCARLD-----GYTLDIWGQGLTVVSS 114

DB 65 LKSRVITSDTSKNQVSLKLSVTAADTAVYCARVLDYDYGSGASDYGQGLTVVSS 123

RESULT 6

ABP45983

ID ABP45983 standard; Protein; 252 AA.

XX AC ABP45983;

DT 19-AUG-2002 (first entry)

XX Human BlyS binding scfv SEQ ID 1994.

XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

XX tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antitumour;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

KM common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

PN WO200202641-A1.

PD 10-JUN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR MPI; 2002-114799/15.

XX Antibodies against B lymphocyte Stimulating polypeptides, useful for

PT the diagnosis and treatment of cancers and immune disorders -

PT Claim 1; Page 2779-2780; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antitumour and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
CC and so may be used to detect and quantitate the presence of BlyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BlyS. They may also be
CC administered to treat diseases associated with aberrant BlyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.

XX Sequence 252 AA;

SQ Query Match 82.9%; Score 505; DB 23; Length 252;

Best Local Similarity 78.2%; Pred. No. 7.5e-40;

Matches 93; Conservative 12; Mismatches 8; Indels 6; Gaps 1;

QY 2 ESGPGIVKPAQTLISCAVSGSIRSGYWMIRHPEKGLEWIGYIYHSQNTYNNPSL 61

DB 6 ESGPGIVKPSQTLISLTCTVSGSISGSGYWMIRHPEKGLEWIGYIYSSSTYNNPSL 65

QY 62 KSRIMSVDTSENKPSLRINSVTAAADTAVYCARL-----DGYTLDIWGQGLTVVSS 114

DB 66 KSRVSVSDTSKNQVSLKLSVTAADTAVYCARLPDADYDYGPDYWGQGLTVVSS 124

RESULT 7
AAB62745
ID AAB62745 standard; Protein; 123 AA.
XX
AC AAB62745;
XX
DT 03-APR-2001 (first entry)
XX
DE Human HIV-1 monoclonal antibody SEQ ID NO: 44.
XX
KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW envelope glycoprotein; gp120; diagnosis.
XX
OS Homo sapiens.
XX
PN WO200100678-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000MO-US17327.
XX
PR 30-JUN-1999; 99US-0141701.
XX
PA (US) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Watkins BA, Reitz MS;
XX
DR WPI; 2001-112438/12.
XX
DR N-PSDB; AAF29046.
XX
PT Novel human monoclonal antibody immunoreactive with human
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal -
XX
PS Claim 1; Page 50; 81pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection.
XX
SQ Sequence 123 AA;
XX
Query Match 82.4%; Score 502; DB 22; Length 123;
Best Local Similarity 79.5%; Pred. No. 6.6e-40;
Matches 93; Conservative 11; Mismatches 9; Indels 4; Gaps 1;
XX
QY 2 ESGPGLVPAQTLISCAVSGSIRSGYMSWIRQHPGKLEWIGYIHSGNTYINPSL 61
DB 7 ESGPGLVPAQTLISCAVSGSIRSGYMSWIRQHPGKLEWIGYIHSGNTYINPSL 66
QY 62 KSRIAMSVDTSENKPSLRLNSTADTAVYCARL---LDGYTLIDWGQTLVTVSS 114
DB 67 KSRIAMSVDTSENKPSLRLNSTADTAVYCARAAYCGGDSFDYWGQTLVTVSS 123
XX
RESULT 8
AAB19829
ID AAB19829 standard; Protein; 251 AA.
XX
AC AAB19829;
XX
DT 10-APR-2003 (first entry)
XX
DE Human VEGF-2 related protein SEQ ID No 75.
XX
KW Cytostatic; cardiant; cardiovascular; antiinflammatory; antithrombotic;
KW antidiabetic; ophthalmological; antiallergic;
KW immunosuppressive; dermatological; antipruritic; vulnary; antibody;
KW CDR region; VH domain; VL domain; immunospecific; VEGF-2; cancer;
XX

XX
KW proliferative disorder; cardiovascular disorder; arrhythmia;
KW cerebrovascular disorder; cerebral anoxia; inflammatory disease;
KW infectious disease; autoimmune disease; rheumatoid arthritis;
KW Systemic Lupus Erythematosus; allergy; diabetic retinopathy; psoriasis;
KW angiogenesis; wound healing; vascular tissue repair; human.
XX
OS Homo sapiens.
XX
PN WO200283704-A1.
XX
PD 24-OCT-2002.
XX
PF 12-APR-2002; 2002WO-US11474.
XX
PR 13-APR-2001; 2001US-283385P.
XX
PR 24-JAN-2002; 2002US-350366P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Albert VR, Ruben SM, Wager RE;
XX
DR WPI; 2003-092991/08.
XX
PT New isolated polynucleotide encoding an antibody which inhibits a
PT VEGF-2 polypeptide, useful for diagnosing, treating or preventing
PT diseases associated with aberrant VEGF-2 expression or function, e.g.
PT cancer or inflammation -
XX
PS Disclosure; Page 385-386; 425pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding a first
CC antibody at least 95-100% identical to a second antibody comprising an
CC amino acid sequence selected from at least one, two or three CDR
CC region(s) of a VH or VL domain where the first antibody
CC immunospecifically inhibits a VEGF-2 polypeptide. The isolated
CC polynucleotide is useful in diagnosing, treating, preventing, prognosing,
CC ameliorating or monitoring diseases associated with aberrant VEGF-2 or
CC VEGF-2 receptor expression or lack of VEGF-2 or VEGF-2 receptor function,
CC such as cancer and other proliferative disorders, cardiovascular
CC disorders (arrhythmias), cerebrovascular disorders (e.g. cerebral
CC anoxia), inflammatory diseases, infectious diseases, autoimmune diseases
CC (e.g. Rheumatoid arthritis, Systemic Lupus Erythematosus, allergies),
CC diabetic retinopathy or psoriasis. The polynucleotide, polypeptide and
CC antibodies may also be used to stimulate angiogenesis, wound healing, and
CC promoting vascular tissue repair. The polynucleotide and polypeptide may
CC also be used for in vitro purposes related to scientific research,
CC synthesis of DNA and manufacture of DNA vectors, and for the production
CC of diagnostics and therapeutics to treat human diseases. This sequence
CC represents a human VEGF-2 related protein of the invention.
XX
SQ Sequence 251 AA;
XX
Query Match 82.2%; Score 500.5; DB 24; Length 251;
Best Local Similarity 79.7%; Pred. No. 2e-39;
Matches 94; Conservative 13; Mismatches 6; Indels 5; Gaps 2;
XX
QY 2 ESGPGLVPAQTLISCAVSGSIRSGYMSWIRQHPGKLEWIGYIHSGNTYINPSL 61
DB 6 ESGPGLVPAQTLISCAVSGSIRSGYMSWIRQHPGKLEWIGYIHSGNTYINPSL 65
QY 62 KSRIAMSVDTSENKPSLRLNSTADTAVYCAR---LDGYTLIDWGQTLVTVSS 114
DB 66 KSRIAMSVDTSENKPSLRLNSTADTAVYCARQKVTGIGGFDLWGRGLTVTVSS 123
XX
RESULT 9
AAB62775
ID AAB62775 standard; Protein; 120 AA.
XX
AC AAB62775;
XX
DT 03-APR-2001 (first entry)
XX

DE Human HIV-1 monoclonal antibody SEQ ID NO: 74.
XX
XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KM envelope glycoprotein; gp120; diagnosis.
XX
XX Homo sapiens.
XX
XX MO200100678-A1.
XX
XX 04-JUN-2001.
XX
XX 23-JUN-2000; 2000WO-US17327.
XX
XX 30-JUN-1999; 99US-0141701.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Watkins BA, Reitz MS;
XX
XX WPI: 2001-112438/12.
XX
XX N-PSDB; AAF29076.
XX
XX Novel human monoclonal antibody immunoreactive with human
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal -
XX
XX Claim 1; Page 69; 81pp; English.
XX
XX The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection.
XX
XX Sequence 120 AA;
SQ
Query Match 82.0%; Score 499.5; DB 22; Length 120;
Best Local Similarity 81.0%; Pred. No. 1.1e-39;
Matches 94; Conservative 12; Mismatches 5; Indels 5; Gaps 2;
QY 2 ESGPGLVKKPAQTLSLSCAVSGSIRSGYWSMIRQHPKGLKLEWIGYIYHSGNTYYPSTL 61
DB 7 ESGPGLVKKPQSTLSLCTVSGSISGQYWSMIRQHPKGLKLEWIGYIYHSGNTYYPSTL 66
QY 62 KSRVITSDTSKQPSLRINSVTAAADTAAYVYCARLDDGYTLIDWGGTLVTVSS 114
DB 67 KSRVITSDTSKQPSLRINSVTAAADTAAYVYCARGVVDMF--DPWGGGTLVTVSS 120
RESULT 10
ID AAB36206 standard; protein; 473 AA.
AC AAB36206;
XX
XX 15-FEB-2001 (first entry)
XX
XX Human immune system associated protein HISAP-4.
DE Human immune system associated protein HISAP-4.
XX
XX Human; immune system associated protein; HISAP-4; immune disorder;
KM infection; autoimmune disease; cancer.
XX
XX Homo sapiens.
XX
XX US6135941-A.
XX
XX 24-OCT-2000.
XX
XX 27-MAR-1998; 98US-0049672.
XX
XX 27-MAR-1998; 98US-0049672.
XX
XX (INCY-) INCYTE PHARM INC.
PA

XX
XX Tang YT, Yue H, Lai P, Corley NC, Guegler KJ, Baughn MR;
PI Hillman JL, Au-Young J;
XX
XX WPI: 2001-030926/04.
XX
XX N-PSDB; AAC65522.
XX
XX New human immune system associated proteins (HISAP) and polynucleotides
PT encoding the HISAP, useful for diagnosing, treating or preventing
PT immune or cell proliferative disorders or infections -
XX
XX Claim 1; Column 53-56; 54pp; English.
XX
XX The present invention provides the coding and protein sequences for a
CC number of human immune system associated proteins (HISAPs). These can be
CC used in the diagnosis and treatment of various autoimmune disorders,
CC infections and cell proliferation diseases. The diseases include AIDS,
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, arteriosclerosis, cirrhosis and cancer.
XX
XX Sequence 473 AA;
SQ
Query Match 81.9%; Score 499; DB 22; Length 473;
Best Local Similarity 78.2%; Pred. No. 5.5e-39;
Matches 93; Conservative 13; Mismatches 7; Indels 6; Gaps 1;
QY 2 ESGPGLVKKPAQTLSLSCAVSGSIRSGYWSMIRQHPKGLKLEWIGYIYHSGNTYYPSTL 61
DB 25 ESGPGLVKKPSESLKSLSCAVSGSISGQYWSMIRQHPKGLKLEWIGYIYHSGNTYYPSTL 84
QY 62 KSRVITSDTSKQPSLRINSVTAAADTAAYVYCARLDDGYTLIDWGGTLVTVSS 114
DB 85 KSRVITSDTSKQPSLRINSVTAAADTAAYVYCARLDDGYTLIDWGGTLVTVSS 143
RESULT 11
ID AAB45608 standard; protein; 253 AA.
AC AAB45608;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 1619.
DE Human Blys binding scFv SEQ ID 1619.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US19110.
XX
XX 16-JUN-2000; 2000US-212210P.
XX
XX 17-OCT-2000; 2000US-240816P.
XX
XX 16-MAR-2001; 2001US-276248P.
XX
XX 21-MAR-2001; 2001US-277379P.
XX
XX 25-MAY-2001; 2001US-293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX (CANA-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX

DR MPI; 2002-11479/15.
XX
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for
PT the diagnosis and treatment of cancers and immune disorders -
XX
XX Claim 1; Page 2335-2336; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
CC tumor necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineoplastic and anti-AIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
CC and so may be used to detect and quantitate the presence of BlyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BlyS. They may also be
CC administered to treat diseases associated with aberrant BlyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.
XX
XX Sequence 253 AA:
SQ
Query Match 81.9%; Score 498.5; DB 23; Length 253;
Best Local Similarity 77.9%; Pred. No. 3.1e-39;
Matches 95; Conservative 12; Mismatches 6; Indels 9; Gaps 3;
QY 2 ESGPLVLRPAQTLISCAVSGSIRSGGYWMIROHPKGLWIGYIHGNTYNNPSL 61
DB 6 ESGPLVLRPAQTLISCAVSGSIRSGGYWMIROHPKGLWIGYIHGNTYNNPSL 65
QY 62 KSRIASVDTSENKSLRLNSVTADTAAYYCAR----LDG--YT--LDINGGCTLVTV 112
DB 66 KSRVITISIDTSKNQSLKLSVTADTAAYYCVRSYTDILRPTTADADINGKTLTV 125
QY 113 SS 114
DB 126 SS 127
XX
XX RESULT 12
XX ID AAY93713
XX AAY93713 standard; Protein; 172 AA.
XX AC AAY93713;
XX DT 03-OCT-2000 (first entry)
XX DE The heavy chain of immunoglobulin clone 2.1.3.
XX KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
XX hyperimmune disorder; autoimmune disease; diabetes; graft rejection;
XX proliferative disorder; cancer; immunodeficient disorder.
XX OS Homo sapiens.
XX PN WO200037504-A2.
XX PD 29-JUN-2000.
XX PF 23-DEC-1999; 99WO-US30895.
XX PR 23-DEC-1998; 98US-0113647.
XX PA (PF12) PFIZER INC.
XX PA (ABGE-) ABGENIX INC.
XX PI Hanson DC, Neveu MJ, Mueller BE, Hanke JH, Gilman SC, Davis CG,
PI Corvajan JR;

XX
XX MPI; 2000-442647/38.
DR N-PSDB; AAA46876.
XX
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
PT (CTLA-4) containing specified heavy and light chain sequences, useful
PT for treating, e.g. immune disorders -
XX
XX Claim 2; Fig 1G; 157pp; English.
XX
XX The present sequence represents a heavy chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
CC (CTLA-4). Antibodies of the invention are composed of a heavy chain
CC variable region, comprising a modified contiguous sequence from a
CC FRI-FRI sequence encoded by a human VH3-33 family gene. The
CC modifications are contained in CDR1, CDR2 and/or framework regions.
CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
CC immune system to treat hyperimmunity disorders (e.g. autoimmune
CC disease, diabetes and graft rejection) and proliferative disorders
CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
CC immune system to up-regulate immunodeficient disorders.
XX
XX Sequence 172 AA:
SQ
Query Match 81.4%; Score 496; DB 21; Length 172;
Best Local Similarity 79.8%; Pred. No. 3.5e-39;
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;
QY 3 SGPGVLRPAQTLISCAVSGSIRSGGYWMIROHPKGLWIGYIHGNTYNNPSL 62
DB 1 SGPGVLRPAQTLISCAVSGSIRSGGYWMIROHPKGLWIGYIHGNTYNNPSL 60
QY 63 SRIMASVDTSENKSLRLNSVTADTAAYYCARLDG--YTLDINGGCTLVTVSS 114
DB 61 SRVITISIDTSKNQSLKLSVTADTAAYYCARSDGYGIDWGGCTTVTVSS 114
XX
XX RESULT 13
XX ID AAB62765
XX AAB62765 standard; Protein; 122 AA.
XX AC AAB62765;
XX DT 03-APR-2001 (first entry)
XX DE Human HIV-1 monoclonal antibody SEQ ID NO: 64.
XX KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
XX envelope glycoprotein; gp120; diagnosis.
XX OS Homo sapiens.
XX PN WO200100678-A1.
XX PD 04-JAN-2001.
XX PF 23-JUN-2000; 2000WO-US17327.
XX PR 30-JUN-1999; 99US-0141701.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PA Watkins BA, Reitz MS;
XX PI
XX MPI; 2001-112438/12.
DR N-PSDB; AAF29066.
XX
XX Novel human monoclonal antibody immunoreactive with human
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal -
XX
XX Claim 1; Page 63; 81pp; English.

XX The present invention provides the protein and coding sequences for the
 CC variable regions of human monoclonal antibodies which are immunoreactive
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
 CC These can be used in diagnosis and therapy of HIV-1 infection.

SQ Sequence 122 AA;

Query Match 81.4%; Score 495.5; DB 22; Length 122;
 Best Local Similarity 80.2%; Pred. No. 2,7e-39;
 Matches 93; Conservative 11; Mismatches 9; Indels 3; Gaps 1;

QY 2 ESGPGVLPQATLSTLSCAVSGSIRSGYWSMIRQHPGKLEWIGYIYHSGNTYYPSTL 61
 Db 7 ESGPGVLPKSQLTSLCTVSGSISGGYWSMIRQHPGKLEWIGYIYHSGNTYYPSTL 66

QY 62 KSRIAMSVDTSENKFSRLNLSVTADTAVYYCAR---LDGYTLDIWGOGTLVTVSS 114
 Db 67 KSRVTTISVDTSKNPSLKLSVTADTAVYYCARDLRLDSTGLCYWGRGTLVTVSS 122

RESULT 14

AAU81275
 ID AAU81275 standard; Protein; 129 AA.

AAU81275;

09-APR-2002 (first entry)

Human t-rkC antibody heavy chain variable region #3.

Human; mouse; anti-t-rkC agonist monoclonal antibody; t-rkC; antibody;
 t-rkA; t-rkB; cisplatin-induced neuropathy; pyridoxine-induced neuropathy;
 peripheral neuropathy; diabetic neuropathy; neurodegenerative disease;
 large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour;
 nerve cell injury; blood cell disorder; leukopenia; eosinopenia; wound;
 basopenia; lymphopenia; monocytopenia; neutropenia; cancer; ulcer;
 Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
 sickle cell disease; cardiac ischaemia; cerebrovascular disorder;
 cellular degeneration; gene therapy.

Homo sapiens.

WO200198361-A2.

27-DEC-2001.

22-JUN-2001; 2001WO-US20153.

22-JUN-2000; 2000US-213141P.

05-OCT-2000; 2000US-238319P.

(GETH) GENENTECH INC.

Devaux B, Hongo JS, Presta LG, Shelton DL;

WPI; 2002-130790/17.

N-PSDB; ABR24410.

Novel anti-t-rkC agonist monoclonal antibody useful for treating

PT neurodegenerative disease, shows no significant cross-reactivity with

PT t-rkA/t-rkB, and recognizes epitope in domain 5 of t-rkC -

Example 1; Fig 9; 121p; English.

The invention relates to an anti-t-rkC agonist monoclonal antibody which
 CC shows no significant cross-reactivity with t-rkA or t-rkB, and recognizes
 CC an epitope in domain 5 of t-rkC. The antibodies of the invention are
 CC effective in the treatment of cisplatin- or pyridoxine-induced
 CC neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre
 CC sensory neuropathy, neurodegenerative disease including amyotrophic
 CC lateral sclerosis, nerve cell injuries, disorders of insufficient blood
 CC cells such as leukopenia including eosinopenia, basopenia,

CC Lymphopenia, monocytopenia, neutropenia, Alzheimer's disease,
 CC Parkinson's disease, Huntington's disease and tumours. The sequences are
 CC also useful for inducing angiogenesis for treating wounds, ulcers and
 CC diabetic complications of sickle cell disease, for treating cardiac
 CC ischaemia and cerebrovascular disorders and in the diagnosis of diseases
 CC involving cellular degeneration. Sequences AAU81229-AAU81284 represent
 CC human and mouse anti-t-rkC agonist monoclonal antibodies and antibody
 CC fragments of the invention.

SQ Sequence 129 AA;

Query Match 81.0%; Score 493.5; DB 23; Length 129;
 Best Local Similarity 77.0%; Pred. No. 4,4e-39;
 Matches 94; Conservative 10; Mismatches 9; Indels 9; Gaps 2;

QY 2 ESGPGVLPQATLSTLSCAVSGSIRSGYWSMIRQHPGKLEWIGYIYHSGNTYYPSTL 61
 Db 7 ESGPGVLPKSQLTSLCTVSGSISGGYWSMIRQHPGKLEWIGYIYHSGNTYYPSTL 66

QY 62 KSRIAMSVDTSENKFSRLNLSVTADTAVYYCAR-----LDGY--TLDIWGOGTLVTV 112
 Db 67 KSRVTTISVDTSKNPSLKLSVTADTAVYYCARERIAAGADYYNGLDVWGOGTLVTV 126

QY 113 SS 114

Db 127 SS 128

RESULT 15

AAAB30584
 ID AAAB30584 standard; Protein; 126 AA.

AAAB30584;

19-MAR-2001 (first entry)

A human variable heavy chain region of anti-IgB antibody.

Anti-idiotypic antibody; C-epsilon3 region; immunoglobulin E; IgE;
 KW anti-IgB antibody; mimobody; vaccine; allergy; asthma; atopic dermatitis;
 KW rhinitis; chronic urticaria; food allergy; IgE-mediated disease;
 KW passive immunisation.

Homo sapiens.

Key Location/Qualifiers

FT Region 30..37 /note= "complementarity determining region 1"

FT Region 51..67 /note= "complementarity determining region 2"

FT Region 100..115 /note= "complementarity determining region 3"

PN WO200063252-A1.

26-OCT-2000.

12-APR-2000; 2000WO-EP03288.

14-APR-1999; 99GB-0008533.

(NOVS) NOVARTIS AG.

(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

Kricek F, Stadler B, Vogel M;

WPI; 2000-687161/67.

N-PSDB; AAC62336.

Novel anti-idiotypic antibody against antibodies which inhibit binding
 PT of immunoglobulin E to its high affinity receptor, useful in vaccines
 PT for treating diseases such as allergy, rhinitis, atopic dermatitis -

PS Claim 4; Fig 5c; 73pp; English.

XX The present sequence represents a human variable heavy chain region of
CC an anti-idiotypic antibody that interferes with the binding of the
CC C-epsilon3 region of immunoglobulin (IgE) to the high affinity receptor
CC for IgE, i.e. and anti-IgE antibody. Such an antibody is referred to
CC as a mAbody. The anti-IgE antibody fragment is used as a vaccine, and
CC in particular asthma, atopic dermatitis, rhinitis, chronic urticaria and
CC food allergies. It is also used to treat IgE-mediated diseases. It is
CC also used for raising polyclonal or monoclonal antibodies. The polyclonal
CC or monoclonal antibodies obtained are useful for treating IgE-mediated
CC diseases by passive immunisation.

XX Sequence 126 AA;

Query Match 80.5%; Score 490; DB 21; Length 126;

Best Local Similarity 75.4%; Pred. No. 9.2e-39;

Matches 92; Conservative 11; Mismatches 11; Indels 8; Gaps 1;

OY 1 LESGPGLYKPAQTLSLSCAVSGSGSIRSGGYWSWIRHPGKLEWIGYIYHSGNTYNPS 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 5 LESGPGLYKPSPTLSLTCTVSGSGSISG3YWTWIRORPGKLEWIGYIYSGSTYNPS 64
OY 61 LKSRIAMSVDTSENKESLRINSVTADTAAYVYCARLDG-----YTLDIWGQGLVTV 112
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 65 LKSRIAMSVDTSENKESLRINSVTADTAAYVYCARERGETGLYPYIYIDWGTGTIVTV 124
OY 113 SS 114
|||
Db 125 SS 126

Search completed: February 10, 2004, 18:36:08
Job time : 63.3727 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 18:39:30 ; Search time 26.2545 Seconds
(without alignments)
909.160 Million cell updates/sec

Title: US-10-027-725A-7

Perfect score: 609
Sequence: 1 LESGPGLVKPAQTSLSCAV.....RLDGYTLIDWGQGLVTVSS 114 /

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/ECT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/ECTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	609	100.0	114	15	US-10-027-725A-7
2	556	91.3	114	15	US-10-027-725A-9
3	546	88.7	114	15	US-10-027-725A-8
4	519	85.2	122	12	US-10-309-762-147
5	518.5	85.1	121	12	US-10-309-762-152
6	517.5	85.0	125	12	US-10-309-762-11
7	514.5	84.5	121	12	US-10-309-762-151
8	512	84.1	118	12	US-10-309-762-138
9	512	84.1	120	12	US-10-309-762-133
10	512	84.1	120	12	US-10-309-762-144
11	509.5	83.7	123	12	US-10-309-762-12
12	508.5	83.5	123	12	US-10-309-762-10
13	508.5	83.5	123	12	US-10-309-762-18
14	508.5	83.5	123	12	US-10-309-762-19
15	508.5	83.5	125	12	US-10-309-762-8

16	508.5	83.5	125	12	US-10-309-762-16	Sequence 16, Appl
17	506.5	83.2	119	12	US-10-309-762-131	Sequence 131, App
18	506.5	83.0	119	12	US-10-309-762-140	Sequence 140, App
19	505	82.9	252	11	US-09-880-748-1994	Sequence 1994, App
20	504.5	82.8	125	12	US-10-309-762-153	Sequence 153, App
21	504	82.8	120	12	US-10-309-762-139	Sequence 139, App
22	503.5	82.7	127	12	US-10-309-762-14	Sequence 14, Appl
23	503	82.6	124	12	US-10-309-762-75	Sequence 75, Appl
24	503	82.6	143	12	US-10-309-762-96	Sequence 96, Appl
25	501.5	82.3	117	12	US-10-330-613-13	Sequence 13, Appl
26	501.5	82.3	117	12	US-10-330-613-13	Sequence 13, Appl
27	500.5	82.2	251	12	US-10-120-414-75	Sequence 75, Appl
28	498.5	81.9	253	11	US-09-880-748-1619	Sequence 1619, Ap
29	497	81.6	110	12	US-10-309-762-17	Sequence 74, Appl
30	497	81.6	121	12	US-10-308-817-137	Sequence 137, App
31	496.5	81.5	123	12	US-10-309-762-17	Sequence 17, Appl
32	496	81.4	172	15	US-10-153-382-21	Sequence 21, Appl
33	495.5	81.4	123	12	US-10-309-762-9	Sequence 9, Appl
34	494.5	81.2	119	12	US-10-330-613-25	Sequence 25, Appl
35	494.5	81.2	119	12	US-10-330-530-25	Sequence 25, Appl
36	493	81.0	221	11	US-09-972-656-80	Sequence 80, Appl
37	490	80.5	126	10	US-09-974-449-6	Sequence 6, Appl
38	489.5	80.4	117	12	US-10-330-613-5	Sequence 5, Appl
39	489.5	80.4	117	12	US-10-330-530-5	Sequence 5, Appl
40	489	80.3	118	12	US-10-078-7578-52	Sequence 52, Appl
41	486	79.8	122	12	US-10-309-762-15	Sequence 15, Appl
42	484	79.5	116	12	US-10-309-762-127	Sequence 127, App
43	482.5	79.2	118	12	US-10-308-817-138	Sequence 138, App
44	482	79.1	256	11	US-09-880-748-1607	Sequence 1607, Ap
45	482	79.1	487	9	US-09-800-729-145	Sequence 145, App

ALIGNMENTS

```

US-10-027-725A-7
; Sequence 7, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-725A-7

Query Match      100.0%; Score 609; DB 15; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.8e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LESGPGLVKPAQTSLSCAVGSGSIRSGGYWMSWIRPGKLEWIGYIHSGNTYVPS 60
      |||
DB      1 LESGPGLVKPAQTSLSCAVGSGSIRSGGYWMSWIRPGKLEWIGYIHSGNTYVPS 60
      |||
QY      61 LKSRIASVDTSENKFSIRLNSVTAADTAAYVYCARLDGYTLIDWGQGLVTVSS 114
      |||
DB      61 LKSRIASVDTSENKFSIRLNSVTAADTAAYVYCARLDGYTLIDWGQGLVTVSS 114
      |||

RESULT 2
US-10-027-725A-9
; Sequence 9, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:

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```
APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-9
```

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Query Match          91.3%; Score 556; DB 15; Length 114;
Best Local Similarity 90.4%; Pred. No. 9e-46;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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```
QY 1 LESGPGLVKPAQTLISCAVSGSIRSGGYMSWIRQHPKGLEWIGYIYHSGNTYYNPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 LESGPGLVKPSQTLISLCTVSGSIRSGGYMSWIRQHPKGLEWIGYIYHSGNTYYNPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LKSRIMSVDTSENKESLRINSVTAADTAVYYCARLDGYTLDIWGQGLVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 LKSRIMSVDTSENKESLRINSVTAADTAVYYCARLDGYTLDIWGQGLVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 3
US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-8
```

```
Query Match          89.7%; Score 546; DB 15; Length 114;
Best Local Similarity 89.5%; Pred. No. 8.1e-45;
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
```

```
QY 1 LESGPGLVKPAQTLISCAVSGSIRSGGYMSWIRQHPKGLEWIGYIYHSGNTYYNPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 LESGPGLVKPSQTLISLCTVSGSIRSGGYMSWIRQHPKGLEWIGYIYHSGNTYYNPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LKSRIMSVDTSENKESLRINSVTAADTAVYYCARLDGYTLDIWGQGLVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 LKSRIMSVDTSENKESLRINSVTAADTAVYYCARLDGYTLDIWGQGLVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 4
US-10-309-762-147
; Sequence 147, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
```

```
CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-147
```

```
Query Match          85.2%; Score 519; DB 12; Length 122;
Best Local Similarity 81.2%; Pred. No. 3.3e-42;
Matches 95; Conservative 12; Mismatches 6; Indels 4; Gaps 1;
```

```
QY 2 ESGPGLVKPAQTLISCAVSGSIRSGGYMSWIRQHPKGLEWIGYIYHSGNTYYNPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 6 ESGPGLVKPSQTLISLCTVSGSIRSGGYMSWIRQHPKGLEWIGYIYHSGNTYYNPSL 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 KSRIMSVDTSENKESLRINSVTAADTAVYYCAR----LDGYTLDIWGQGLVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 66 KSRVITISVDTSENKPSLRINSVTAADTAVYYCARYYDILTYGMDVWGQGLVTVSS 122
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 5
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-152
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```
Query Match          85.1%; Score 518.5; DB 12; Length 121;
Best Local Similarity 81.9%; Pred. No. 3.7e-42;
Matches 95; Conservative 11; Mismatches 7; Indels 3; Gaps 1;
```

```
QY 2 ESGPGLVKPAQTLISCAVSGSIRSGGYMSWIRQHPKGLEWIGYIYHSGNTYYNPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 6 ESGPGLVKPSQTLISLCTVSGSIRSGGYMSWIRQHPKGLEWIGYIYHSGNTYYNPSL 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 KSRIMSVDTSENKESLRINSVTAADTAVYYCARLD---GYTLDIWGQGLVTVSS 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 66 KSRVITISVDTSENKPSLRINSVTAADTAVYYCARYYDILTYGMDVWGQGLVTVSS 121
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 6
US-10-309-762-11
; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
```

FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-11

Query Match 85.0%; Score 517.5; DB 12; Length 125;
Best Local Similarity 81.7%; Pred. No. 4.7e-42;
Matches 98; Conservative 9; Mismatches 6; Indels 7; Gaps 2;

Oy 2 ESGGGLVPAQTLISCAVSGSIRSGYWSWIRHPGKLEWIGYTHSGNTYVNSL 61
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGGGLVPSQTLISCTVSGGSISGGYWSWIRHPGKLEWIGYTHSGNTYVNSL 65
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 62 KSRIAMSVDSSENKFSRLNSVTADTAIVYYCARL---LDGY--TLDIWGGTLVTVSS 114
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRIATISVDTSKNQFSLKLSVTADTAIVYYCARTYDFLGTGYPADPDIMWGQTLVTVSS 125
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
US-10-309-762-151
Sequence 151, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudus, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 151
LENGTH: 121
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-151

Query Match 84.5%; Score 514.5; DB 12; Length 121;
Best Local Similarity 81.0%; Pred. No. 8.9e-42;
Matches 94; Conservative 13; Mismatches 6; Indels 3; Gaps 1;

Oy 2 ESGGGLVPAQTLISCAVSGSIRSGYWSWIRHPGKLEWIGYTHSGNTYVNSL 61
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Db 6 ESGGGLVPSQTLISCTVSGGSISGGYWSWIRHPGKLEWIGYTHSGNTYVNSL 65
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 62 KSRIAMSVDSSENKFSRLNSVTADTAIVYYCARL---DGYTLDIWGGTLVTVSS 114
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRIATISVDTSKNQFSLKLSVTADTAIVYYCARLFLMGDMVWGQTLVTVSS 121
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
US-10-309-762-138
Sequence 138, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudus, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 138
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-138

Query Match 84.1%; Score 512; DB 12; Length 118;
Best Local Similarity 83.2%; Pred. No. 1.5e-41;
Matches 94; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Oy 2 ESGGGLVPAQTLISCAVSGSIRSGYWSWIRHPGKLEWIGYTHSGNTYVNSL 61
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGGGLVPSQTLISCTVSGGSISGGYWSWIRHPGKLEWIGYTHSGNTYVNSL 65
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 62 KSRIAMSVDSSENKFSRLNSVTADTAIVYYCARL---LDGY--TLDIWGGTLVTVSS 114
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRIATISVDTSKNQFSLKLSVTADTAIVYYCARTYDFLGTGYPADPDIMWGQTLVTVSS 118
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
US-10-309-762-13
Sequence 13, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudus, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-13

Query Match 84.1%; Score 512; DB 12; Length 120;
Best Local Similarity 81.9%; Pred. No. 1.5e-41;
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;

Oy 2 ESGGGLVPAQTLISCAVSGSIRSGYWSWIRHPGKLEWIGYTHSGNTYVNSL 61
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 ESGGGLVPSQTLISCTVSGGSISGGYWSWIRHPGKLEWIGYTHSGNTYVNSL 65
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Oy 62 KSRIAMSVDSSENKFSRLNSVTADTAIVYYCARL---LDGY--TLDIWGGTLVTVSS 114
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRIATISVDTSKNQFSLKLSVTADTAIVYYCARL---DGYTLDIWGGTLVTVSS 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
US-10-309-762-144
Sequence 144, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudus, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael

```

; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-144
```

```

Query Match      84.1%; Score 512; DB 12; Length 120;
Best Local Similarity 81.9%; Pred. No. 1.5e-41;
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;
```

```

QY 2 ESGPGLVKAQTLISLSCAVSGSIRSGGYWMIROHPGKLEWIGIYHSGNTYNNPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
    ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 6 ESGPGLVKPSQTLSTCTVSGSISGGYWSMIROHPGKLEWIGIYHSGNTYNNPSL 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 KSRIVSVDTSENKFSRLNSVTAAADTAAYVYCARLDGTY---LDINGQGLTVTVSS 114
    ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 66 KSRVITISVDTSKNQSFKLSSTVAADTAAYVYCARLDGTYNMYFDIMGRGLTVTVSS 120
```

```

RESULT 11
US-10-309-762-12
; Sequence 12, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-12
```

```

Query Match      83.7%; Score 509.5; DB 12; Length 123;
Best Local Similarity 78.8%; Pred. No. 2.7e-41;
Matches 93; Conservative 13; Mismatches 7; Indels 5; Gaps 1;
```

```

QY 2 ESGPGLVKAQTLISLSCAVSGSIRSGGYWMIROHPGKLEWIGIYHSGNTYNNPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
    ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 6 ESGPGLVKPSQTLSTCTVSGSISGGYWSMIROHPGKLEWIGIYHSGNTYNNPSL 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 KSRIVSVDTSENKFSRLNSVTAAADTAAYVYCARLDGTYLDIMQGLTVTVSS 114
    ||::|||:|||||:|||||:|||||:|||||:|||||:|||||
DB 66 KSRVITISVDTSKNQSFKLSSTVAADTAAYVYCARLDGTYNMYFDIMQGLTVTVSS 123
```

```

RESULT 12
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
```

```

; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10
```

```

Query Match      83.5%; Score 508.5; DB 12; Length 123;
Best Local Similarity 80.5%; Pred. No. 3.4e-41;
Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;
```

```

QY 2 ESGPGLVKAQTLISLSCAVSGSIRSGGYWMIROHPGKLEWIGIYHSGNTYNNPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
    ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 6 ESGPGLVKPSQTLSTCTVSGSISGGYWSMIROHPGKLEWIGIYHSGNTYNNPSL 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 KSRIVSVDTSENKFSRLNSVTAAADTAAYVYCARLDGTYLDIMQGLTVTVSS 114
    ||::|||:|||||:|||||:|||||:|||||:|||||:|||||
DB 66 KSRVITISVDTSKNQSFKLSSTVAADTAAYVYCARAGKTYGSGSYLDIMQGLTVTVSS 123
```

```

RESULT 13
US-10-309-762-18
; Sequence 18, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-18
```

```

Query Match      83.5%; Score 508.5; DB 12; Length 123;
Best Local Similarity 80.5%; Pred. No. 3.4e-41;
Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;
```

```

QY 2 ESGPGLVKAQTLISLSCAVSGSIRSGGYWMIROHPGKLEWIGIYHSGNTYNNPSL 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
    ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 6 ESGPGLVKPSQTLSTCTVSGSISGGYWSMIROHPGKLEWIGIYHSGNTYNNPSL 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 KSRIVSVDTSENKFSRLNSVTAAADTAAYVYCARLDGTYLDIMQGLTVTVSS 114
    ||::|||:|||||:|||||:|||||:|||||:|||||:|||||
DB 66 KSRVITISVDTSKNQSFKLSSTVAADTAAYVYCARERVDYDYIYGLDIMQGLTVTVSS 123
```

```

RESULT 14
US-10-309-762-19
; Sequence 19, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
```

APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 19
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-19

Query Match 83.5%; Score 508.5; DB 12; Length 123;
Best Local Similarity 80.5%; Pred. No. 3.4e-41;
Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;

QY 2 ESGPGLVPAQTLSICAVSGSIRSGYMSIRQHPGKLEWIGIYHSGNTYYNPSL 61
DB 6 ESGPGLVPAQTLSICAVSGSIRSGYMSIRQHPGKLEWIGIYHSGNTYYNPSL 65
QY 62 KSRIMSVDTSENKSLRLNSTYAADTAVYYCAR-----LDGYTLDIWGQGLTVVSS 114
DB 66 KSRVITISVDTSENKSLRLNSTYAADTAVYYCARRRVTDYVYGLDVGQGLTVVSS 123

RESULT 15

US-10-309-762-8
Sequence 8, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Guadas, Jean
APPLICANT: Folcz, Jan
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 8
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-8

Query Match 83.5%; Score 508.5; DB 12; Length 125;
Best Local Similarity 79.2%; Pred. No. 3.4e-41;
Matches 95; Conservative 12; Mismatches 6; Indels 7; Gaps 2;

QY 2 ESGPGLVPAQTLSICAVSGSIRSGYMSIRQHPGKLEWIGIYHSGNTYYNPSL 61
DB 6 ESGPGLVPAQTLSICAVSGSIRSGYMSIRQHPGKLEWIGIYHSGNTYYNPSL 65
QY 62 KSRIMSVDTSENKSLRLNSTYAADTAVYYCAR-----LDGYTLDIWGQGLTVVSS 114
DB 66 KSRVITISVDTSENKSLRLNSTYAADTAVYYCARRTYDILTGYPDAFDIWGQGLTVVSS 125

Search completed: February 10, 2004, 19:03:02
Job time : 33.2545 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:32:44 : Search time 11.7455 Seconds

(without alignments)
410.664 Million cell updates/sec

Title: US-10-027-725A-7

Sequence: 1 LESGPGLVKAQTSLSCAV.....RLDGTLDIMGQGLVTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfill1est1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	499	81.9	473	3	US-09-049-672A-4
2	471.5	77.4	119	1	US-08-360-125-5
3	471.5	77.4	119	2	US-08-450-578-5
4	471.5	77.4	119	2	US-09-017-628-5
5	471.5	77.4	119	2	US-09-014-880-5
6	471.5	77.4	119	4	US-09-025-769B-39
7	471.5	77.4	119	4	US-09-025-769B-65
8	471.5	77.4	119	4	US-08-450-363-5
9	466	76.5	122	1	US-08-360-125-11
10	466	76.5	122	2	US-08-450-578-11
11	466	76.5	122	2	US-09-017-628-11
12	466	76.5	122	2	US-09-014-880-11
13	466	76.5	122	2	US-08-450-363-11
14	455	74.7	118	4	US-09-025-769B-25
15	453	74.4	118	4	US-08-545-809A-116
16	446.5	73.3	250	4	US-10-039-785-50
17	445	73.1	244	4	US-08-918-148-79
18	442.5	72.7	142	2	US-08-480-774A-2
19	438	71.9	278	3	US-08-260-527-3
20	429.5	70.5	119	2	US-08-652-816A-10
21	429	70.4	150	4	US-09-582-337-14
22	427	70.1	118	4	US-09-343-698-6
23	425.5	69.9	476	4	US-08-487-550-12
24	425.5	69.9	476	4	US-09-526-098-12
25	424	69.6	118	3	US-08-545-809A-142
26	422.5	69.4	98	1	US-08-478-039-75
27	422.5	69.4	98	1	US-08-476-349A-75

28	422	69.3	126	1	US-08-276-852-142	Sequence 142, App
29	422	69.3	126	1	US-08-899-575-142	Sequence 142, App
30	422	69.3	126	5	US-08-899-575-142	Sequence 142, App
31	422	69.3	126	5	PCT-US95-08743-142	Sequence 142, App
32	420.5	69.0	124	1	US-08-478-039-78	Sequence 78, App
33	420.5	69.0	124	1	US-08-476-349A-78	Sequence 78, App
34	420	69.0	832	3	US-08-630-820-7	Sequence 37, App
35	419.5	68.9	219	4	US-09-460-384-37	Sequence 27, App
36	418.5	68.7	96	3	US-08-851-362D-27	Sequence 44, App
37	418.5	68.7	117	3	US-08-851-362D-44	Sequence 44, App
38	418.5	68.7	123	4	US-08-793-450-4	Sequence 4, App
39	418.5	68.7	472	4	US-08-793-450-8	Sequence 8, App
40	418	68.6	244	4	US-10-039-785-44	Sequence 44, App
41	415	68.1	118	3	US-08-545-809A-123	Sequence 123, App
42	414	68.0	119	1	US-08-478-039-77	Sequence 77, App
43	414	68.0	119	1	US-08-476-349A-77	Sequence 77, App
44	410.5	67.4	467	3	US-08-523-894-8	Sequence 8, App
45	410.5	67.4	467	3	US-08-523-894-10	Sequence 10, App

ALIGNMENTS

RESULT 1
US-09-049-672A-4
Sequence 4, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Yang, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREMITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PR-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANCYTUT01

CLONE: 1513264
US-09-049-672A-4
Query Match 81.9%; Score 499; DB 3; Length 473;
Best Local Similarity 78.2%; Pred. No. 2.7e-43;
Matches 93; Conservative 13; Mismatches 7; Indels 6; Gaps 1;
QY 2 ESGPGVVKPAQTLISCAVSGGSIKSGGYWMIROHPGKLEWIGYIYHSGNTYYPSTL 61
DB 25 ESGPGVVKPSETSLTCAVSGGSIKSGGYWMIROHPGKLEWIGYIYHSGNTYYPSTL 84
62 KSRIMSVDTSENKFSRLNSVTADTAVYVCARDL-----GYTLDIWGQGLTVTVSS 114
DB 85 KSRVTSIDTSKQFSLKLSVTADTAVYVCARDVGLRGNGYGMVWGQGLTVTVSS 143
RESULT 2
US-08-360-125-5
Sequence 5, Application US/08360125
Patent No. 5767246
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: YOKO HIRAKAWA
APPLICANT: No. 5767246shiko ITO
APPLICANT: Kazuhiko NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08360,125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLER:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENE:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-5
Query Match 77.4%; Score 471.5; DB 1; Length 119;
Best Local Similarity 75.9%; Pred. No. 3.5e-41;
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;
QY 2 ESGPGVVKPAQTLISCAVSGGSIKSGGYWMIROHPGKLEWIGYIYHSGNTYYPSTL 61
DB 6 ESGPGVVKPSETSLTCAVSGGSIKSGGYWMIROHPGKLEWIGYIYHSGNTYYPSTL 65
62 KSRIMSVDTSENKFSRLNSVTADTAVYVCARDL-----RLDGYTLDIWGQGLTVTVSS 114
DB 66 KSRVTSIDTSKQFSLKLSVTADTAVYVCARDSTRLG--ADYWGQGLTVTVSS 119
RESULT 3
US-08-450-578-5
Sequence 5, Application US/08450578
Patent No. 5837845
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: YOKO HIRAKAWA
APPLICANT: No. 5837845shiko ITO
APPLICANT: Kazuhiko NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL LINE: antibody GAH
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-5

Query Match 77.4%; Score 471.5; DB 2; Length 119;
Best Local Similarity 75.9%; Pred. No. 3.5e-41;
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

QY 2 ESGPGLVAPQATLSLSCAVSGSIRSGYWSWIRHFGKLEWIGYIYHSGNTYNSL 61
DB 6 ESGPGLVAPQATLSLSCAVSGSIRSGYWSWIRHFGKLEWIGYIYHSGNTYNSL 65

QY 62 KSRIMSVDTSENKSLRLNSVTADTAIVYCA---RLDGYTLIDWGCTLVTVSS 114

DB 66 KSRVTLSDTSKQFSLKSLTAADTAIVYCASTRLRG--ADYWGQGTWTVSS 119

RESULT 4
US-09-017-628-5
Sequence 5, Application US/09017628
Patent No. 5990287
GENERAL INFORMATION:
APPLICANT: HOSOKAWA, Saiko
APPLICANT: TAGAWA, Toshiaki
APPLICANT: HIRAKAWA, Yoko
APPLICANT: ITO, No. 5990287iniko
APPLICANT: NAGAIKE, Kazuhiko
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
FILE REFERENCE: 177/527361KH
CURRENT FILING DATE: 1998-02-02
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 119
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-5

Query Match 77.4%; Score 471.5; DB 2; Length 119;
Best Local Similarity 75.9%; Pred. No. 3.5e-41;
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

QY 2 ESGPGLVAPQATLSLSCAVSGSIRSGYWSWIRHFGKLEWIGYIYHSGNTYNSL 61
DB 6 ESGPGLVAPQATLSLSCAVSGSIRSGYWSWIRHFGKLEWIGYIYHSGNTYNSL 65

QY 62 KSRIMSVDTSENKSLRLNSVTADTAIVYCA---RLDGYTLIDWGCTLVTVSS 114
DB 66 KSRVTLSDTSKQFSLKSLTAADTAIVYCASTRLRG--ADYWGQGTWTVSS 119

RESULT 5
US-09-014-880-5
Sequence 5, Application US/09014880
Patent No. 5990297
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995
PRIOR APPLICATION DATA:

CELL TYPE: Hybridoma producing

```

CLASSIFICATION: 424
PRIOR APPLICATION DATA:

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OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-11

Query Match 76.5%; Score 466; DB 2; Length 122;
Best Local Similarity 75.2%; Pred. No. 1.3e-40;
Matches 88; Conservative 13; Mismatches 12; Indels 4; Gaps 2;

QY 2 ESGPGLVPAOTLSLSCAVSGSIRSGGYWMSIRHOGKLEWIGYIHSGNTYYPNSL 61
DB 6 ESGPGLVPAOTLSLSCAVSGSIRSGGYWMSIRHOGKLEWIGYIHSGNTYYPNSL 65

QY 62 KSRIVTSVDTSKNPSLKLSTVTAADTAIVYCAR--LDG--YTLIDWOGGLTVVSS 114
DB 66 KSRIVTSVDTSKNPSLKLSTVTAADTAIVYCARSGYGGYGMVWGGTTVTVSS 122

RESULT 11
US-09-017-628-11
Sequence 11, Application US/09017628
Patent No. 5990287
GENERAL INFORMATION:
APPLICANT: HOSOKAWA, Saiko
APPLICANT: TAGAWA, Yoshiaki
APPLICANT: HIRAKAWA, Yoko
APPLICANT: ITO, No. 5990287ihiko
APPLICANT: NAGAIKE, Kazuhiko
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
FILE REFERENCE: 177/527361KH
CURRENT FILING DATE: 1998-02-02
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 122
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-11

Query Match 76.5%; Score 466; DB 2; Length 122;
Best Local Similarity 75.2%; Pred. No. 1.3e-40;
Matches 88; Conservative 13; Mismatches 12; Indels 4; Gaps 2;

QY 2 ESGPGLVPAOTLSLSCAVSGSIRSGGYWMSIRHOGKLEWIGYIHSGNTYYPNSL 61
DB 6 ESGPGLVPAOTLSLSCAVSGSIRSGGYWMSIRHOGKLEWIGYIHSGNTYYPNSL 65

QY 62 KSRIVTSVDTSKNPSLKLSTVTAADTAIVYCAR--LDG--YTLIDWOGGLTVVSS 114
DB 66 KSRIVTSVDTSKNPSLKLSTVTAADTAIVYCARSGYGGYGMVWGGTTVTVSS 122

RESULT 12
US-09-014-880-11
Sequence 11, Application US/09014880
Patent No. 5990297
GENERAL INFORMATION:

APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 R Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-11

Query Match 76.5%; Score 466; DB 2; Length 122;
Best Local Similarity 75.2%; Pred. No. 1.3e-40;
Matches 88; Conservative 13; Mismatches 12; Indels 4; Gaps 2;

QY 2 ESGPGLVPAOTLSLSCAVSGSIRSGGYWMSIRHOGKLEWIGYIHSGNTYYPNSL 61
DB 6 ESGPGLVPAOTLSLSCAVSGSIRSGGYWMSIRHOGKLEWIGYIHSGNTYYPNSL 65

QY 62 KSRIVTSVDTSKNPSLKLSTVTAADTAIVYCAR--LDG--YTLIDWOGGLTVVSS 114
DB 66 KSRIVTSVDTSKNPSLKLSTVTAADTAIVYCARSGYGGYGMVWGGTTVTVSS 122

RESULT 13
US-08-450-363-11
Sequence 11, Application US/08450363
Patent No. 6436434
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 6436434ihiko ITO
APPLICANT: Kazuhiko NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

TITLE OF INVENTION: Cell Membrane
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wenderoth, Lind & Ponack
 STREET: 805 Fifteenth Street, N.W., #700
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/450,363
 FILING DATE: May 25, 1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/360,125
 FILING DATE: December 20, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/905,534
 FILING DATE: June 29, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren M. Cheek, Jr.
 REGISTRATION NUMBER: 33,367
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-8850
 TELEFAX:
 TELEX:
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 122 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEetical:
 ANTI-SENSE:
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM:
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE:
 CELL TYPE: Hybridoma producing human antibody 1-3-1
 ORGANELLE:
 IMMEDIATE SOURCE:
 LIBRARY:
 CLONE:
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT:
 MAP POSITION:
 UNITS:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 PUBLICATION INFORMATION:
 AUTHORS:
 TITLE:
 JOURNAL:
 VOLUME:
 ISSUE:
 PAGES:
 DATE:
 DOCUMENT NUMBER:

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; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-11

Query Match      76.5%; Score 466; DB 4; Length 122;
Best Local Similarity 75.2%; Pred. No. 1,3e-40;
Matches 88; Conservative * 13; Mismatches 12; Indels 4; Gaps 2;

Oy 2 EESGGLVKKPQDTLSLCAVSGGSIRSGGYWSWTRHPHGKLEIGIYHSGNTYYNPSL 61
Db 6 EESGGLVKPSETTSLRTCTVGSGSISSSSYWGWRPPGGKLEIGIYHSGSYYNPSL 65
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
62 KSRFAMVDISENFSEFRILNSVTAPADAVYYCAR--LDG--YTLDINGOGTLTVSS 114
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 66 KSRTITSDISKDFSLKISSVTAPADAVYYCARGSIGGYGMDVWGCGITTVVSS 122

RESULT 14
US-09-025-769B-25
Sequence 25. Application US/09025769B
Patent No. 6300864
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-25

Query Match      74.7%; Score 455; DB 4; Length 118;
Best Local Similarity 77.4%; Pred. No. 1.7e-39;
Matches 89; Conservative 10; Mismatches 12; Indels 4; Gaps 2;

Oy 2 EESGGLVKKPQDTLSLCAVSGGSIRSGGYWSWTRHPHGKLEIGIYHSGNTYYNPSL 61
Db 6 EESGGLVKPSETTSLRTCTVGSGSIS--YYSMWIRPPGGKLEIGIYHSGSYNNPSL 63
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

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OY 62 KSRIAMVDTSSEKSLRLNSTADTADTAVYYCA--RLDGYTLIDIMGOSTLVTVSS 114
 DB 64 KSRVTISVDTSKNGPSLKLSSVTADTADTAVYYCAKGRGGGVFDYMGOSTLVTVSS 118

RESULT 15

US-08-545-809A-116
 ; Sequence 116, Application US/08545809A
 ; Patent No. 6096878
 ; GENERAL INFORMATION:
 ; APPLICANT: Honjo, Tasuku
 ; APPLICANT: Matsuda, Fumihiko
 ; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
 ; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
 ; NUMBER OF SEQUENCES: 145
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson, P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: US
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/545, 809A
 ; FILING DATE: 27-MAR-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/JP93/00603
 ; FILING DATE: 10-MAY-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Freeman, John W.
 ; REGISTRATION NUMBER: 29, 066
 ; REFERENCE/DOCKET NUMBER: 06501/004001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-542-5070
 ; TELEFAX: 617-542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 116:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 118 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-545-809A-116

Query Match 74.4%; Score 453; DB 3; Length 118;
 Best Local Similarity 86.2%; Pred. No. 2.7e-39;
 Matches 81; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

OY 2 ESGGGLVPAOTLISCAVSGSIRSGYVSWIRQHPKGLIEWIGYTHSGNTYVNPSTL 61
 DB 25 ESGGGLVPSQTLSTCTVSGSSISGGYVSWIRQHPKGLIEWIGYTHSGNTYVNPSTL 84
 OY 62 KSRIAMVDTSSEKSLRLNSTADTADTAVYYCAR 95
 DB 85 KSRVTISVDTSKNGPSLKLSSVTADTADTAVYYCAR 118

Search completed: February 10, 2004, 18:42:06
 Job time : 19.7455 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:26:58 ; Search time 11.7455 Seconds
(without alignments)
933.402 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614
Sequence: 1 LESGRLVPSQTSLTCTV.....RSDGTYLDNMCGTLVTSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*

1: pirl:1:1
2: pirl:2:1
3: pirl:3:1
4: pirl:4:1

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	499.5	81.4	135	2	S78051 Ig heavy chain pre
2	495.5	80.7	147	2	S13519 Ig heavy chain V r
3	487	79.3	130	2	S30534 Ig heavy chain V r
4	480.5	78.3	121	2	S44113 Ig heavy chain V r
5	478.5	77.9	140	2	I37782 Ig variable region
6	477.5	77.8	146	2	S09710 Ig heavy chain V r
7	474.5	77.3	116	2	S37456 Ig mu chain - huma
8	474.5	77.3	130	2	S31690 Ig heavy chain V r
9	474	77.2	122	2	S69912 Ig V-D-J region (N
10	473.5	77.1	128	2	S31514 Ig heavy chain - h
11	472.5	77.0	127	2	S19668 Ig heavy chain V r
12	469	76.4	137	2	S31676 Ig heavy chain V r
13	468.5	76.3	133	2	S30530 Ig heavy chain V r
14	465.5	75.8	155	2	S31511 Ig heavy chain - h
15	463.5	75.5	155	2	S31512 Ig heavy chain - h
16	462	75.2	139	2	S31586 Ig heavy chain V r
17	460.5	75.0	146	2	S09711 Ig heavy chain V r
18	460	74.9	145	2	S78055 Ig heavy chain pre
19	459.5	74.8	109	2	PH1673 Ig heavy chain V r
20	457	74.4	110	2	S44110 Ig heavy chain V-D
21	455	74.1	99	2	S26803 Ig heavy chain V r
22	454	73.9	139	2	A41287 Ig heavy chain pre
23	453	73.8	99	2	S26801 Ig heavy chain V r
24	452	73.6	129	2	S44114 Ig heavy chain V r
25	450	73.3	99	2	S26802 Ig heavy chain V r
26	447	72.8	118	2	S20780 Ig heavy chain V r
27	447	72.8	99	2	S12418 Ig heavy chain V r
28	446	72.6	99	2	S12418 Ig heavy chain V r
29	444.5	72.4	139	2	S31696 Ig heavy chain V r

30	443	72.1	118	2	A26340 Ig heavy chain pre
31	442.5	72.1	140	2	A49045 Ig heavy chain V r
32	441.5	71.9	132	2	A38911 Ig heavy chain V r
33	441	71.8	99	2	S26800 Ig heavy chain V r
34	441	71.8	126	2	S47010 Ig heavy chain V4.
35	440.5	71.7	129	1	D2HWA Ig heavy chain V-I
36	440	71.7	97	2	PL0118 Ig heavy chain V-I
37	440	71.7	99	2	S26899 Ig heavy chain V r
38	439.5	71.6	98	2	S12421 Ig heavy chain V r
39	439.5	71.6	140	2	A4770 hypothetical hybr
40	439	71.5	140	2	S78052 Ig heavy chain pre
41	438.5	71.4	123	2	S30529 Ig heavy chain V r
42	438	71.3	120	2	PR0370 Ig mu chain precu
43	437	71.2	124	2	S31684 Ig heavy chain V r
44	435.5	70.9	134	2	S54906 Ig heavy chain V r
45	434.5	70.8	98	2	S26902 Ig heavy chain V r

ALIGNMENTS

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RESULT 1
S78051
Ig heavy chain precursor V-D-J region (clone mab 61VH) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78051; S23716
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78051
A:Molecule type: mRNA
A:Residues: 1-135 <HAR>
A:Cross-references: EMBL:X54437, NID:G37814, PID:CA38306.1, PID:G930117
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404
A:Accession: S23716
A:Molecule type: mRNA
A:Residues: 13-111 <HAW>
A:Cross-references: EMBL:X54437
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-13/Domain: signal sequence (fragment) #status predicted <SIG>
F:14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:27-111/Domain: immunoglobulin homology <IMM>

Query Match      81.4% Score 499.5; DB 2; Length 135;
Best Local Similarity 79.7% Pred. No. 9.3e-38;
Matches 94; Conservative 10; Mismatches 9; Indels 5; Gaps 2;

QY      2  ESGRLVPSQTSLTCTVSGSIRSGYSWVROPKGLWIGNIYHSGNTYPSL 61
DB      18  ESGRLVPSQTSLTCTVSGSIRSGYSWVROPKGLWIGNIYHSGNTYPSL 77
QY      62  KSRITMSVDTSKNHFSLRLTSVTADTAIVVYCAR--SDGYTLDN---WGQGLTVTVSS 114
DB      78  KSRITMSVDTSKNHFSLRLTSVTADTAIVVYCARLGPDDYTLDMVDVWGQGLTVTVSS 135

RESULT 2
S13519
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S13519
R:Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A:Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A:Reference number: S13519; MUID:91187691; PMID:2011536
A:Accession: S13519
```

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-147 <EMBL>
A:Cross-references: EMBL:X65158, NID:g37724, PIDN:CAA39626.1, PID:g37725
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:41-125/Domain: immunoglobulin homology <IIM>

Query Match	80.7%	Score 495.5	DB 2	Length 147	.
Best Local Similarity	80.2%	Pred. NO. 2.3e-37			
Matches 93, Conservative			9, Mismatches 11,	Indels 3,	Gaps 1

```

Oy      2  ESGPGLVKPSQTLSTLCTVSGGSTRGGCYWWSWTRQPPGKGLWGNLYHSGNTYNNPSL 61
          |||||:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      32  ESGPGLVKPSQTLSTLCTVSGGSTRGGCYWWSWTRQPPGKGLWGNLYHSGNTYNNPSL 91

```

Qy	62	KSRTIMSVDTSKNHFSLRLTSTVADTA	VVYCAR---	DGYTL	LDNMGGTL	VTVSS	114
		::	::				
Db	92	KSRTVISVDTSKNQFSLKLTSSVTADTA	VVYCARPLIMFGLFDYMGGTL	VTVSS			147

```

RESULT 3
S30534
Ig heavy chain V region - human
CISpecies: Homo sapiens (man)
CISDate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
CISAccession: S30534

```

submitted to the EMBL Data Library, October 1992
A/Reference number: S30520
A/Accession: S30534

```
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-110 <MAR>
A:Cross-references: EMBL:Z18320
C:Superfamily: immunoglobulin V region; immunoglobulin
C:Keywords: heterotetramer; immunoglobulin
P:15-99/Domain: immunoglobulin homology <IMM>
```

Query Match	79.3%;	Score	487;	DB 2;	Length	130;
Best Local Similarity	76.0%;	Pred.	No. 1.2e-36;			
Matches	95;	Conservative	7;	Mismatches	11;	Indels 12;
						Gaps 2;

```

Qy      2  ESGPGIVKPSQTLSTLCTVSGSIRSGCYWYMWVRQPPGKGLEWIGNITYHSQNTYYNPDL 61
        |||||
Db      6  ESGPGIVKPSQTLSTLCTVSGSIRSSSYWYMWIRQPPGKGLEWIGRITYSSGNTNYPDL 65

```

```

Qy      62  KSRIMSVDSKHNHSELRSTVTAADPAVYYCARSDG-----YT-----LDNMGQETL 109
Db      66  KSRIVISVDSKNOFSLKLSSTTAADPAVYYCARDKGGFWGSGYYTRNSRAADIWGQITM 125

```

QY	110	VTVSS	114
Db	126	VTVSS	130

RESULT 4

ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text change 24-May-2001

R. Hawkins, R. E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T. J.; Stevenson, F. K.; Heutschaer, T. Submitted to the EMBL Data Library, March 1994.

Reference number: S4113
Accession: S4113
Status: preliminary
Molecule type: DNA

A:Cross-references: EMBL:Z13389, NID:g472967; PIDD:CAAB3264.1; PID:g940524
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F;15-99/Domain: immunoglobulin homology <IMM>

Query Match	78.3%	Score	480.5	DB 2	Length	121			
Best Local Similarity	78.4%	Pred. NO.	4.1e-36						
Matches	91	Conservative	9	Mismatches	13	Indels	3	Gaps	2

Qy

2 ESGPGVLVKPSQTLSLTCTVSGGSIRSGGYWWSWTRQPQPKGLEWIGNIYHSGNTYYNPSL
|||||:||||||| | ||| :||| :|||
Ddb

6 ESGPGLVKPSETLSLTCTVSGGISSSYWGWRQPPKGLIEWISSIYYSSGTYYNPSLL

Oy	62 KSRITMSVDTSKNHFSRLTSTVTAADTAVYYCAR-SDGY--TLDNNGQGLTVTVSS	114
	:: ::: :: :	
Ddb	66 KSRVTLSVDTSKNOFSLKLSSVTAADTGYYCSRLSGGYYDFDYNQGTLVTVSS	121

RESULT 5
137782

C:\Species: Homo sapiens (man)
C:\Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C:\Accession: I37782; S25476

A:Reference number: A36876; NCBI:94119917; PMID:82905

A:Residues: 1-140 <PSS>
A:Status: preliminary
A:Molecule type: mRNA
A:Accession: J37782

A: Cross-References: EMBL:AF7506; NID:G3358.1; FID:CA44104.1; FID:G3358.1; Superfamily: immunoglobulin V region; immunoglobulin homology C:46-128/Domain: immunoglobulin homology <IM>

Query Match	77.9%	DS 2	Length 140;
Best Local	Score 478.5;	Pred. No. 7.2e-36;	
Matches	93; Conservative	9; Mismatches	9; Indels 7; Gaps 2

```

QY      2  ESGPGIATKPSSTLSLTCTVSGSIRSGYIYMSWVQPPGKGLEWIGNIYHSGNTIYNPSL  61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      25  ESGPGIATKPSSTLSLTCTVSGSIS--YMSWIRQPPGKGLEWIGIYIYSGSTININPSL  82

```

```

Qy      62 KSRRTMSVDTSKIHFSLRITSVTADTAIVYCCASD-----GYTLDDNWGGTLVTVSS 114
        |||::|||  |||::|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      63 KSRVTISVDTSKQFSLKLSVTIADTAIVYCCARNHSSSWYGRYFDYMGGTLVTVSS 140

```

RESULT 6
S09710

C:Species: Homo sapiens (man)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S09710

Biochem. J. 268, 135-140, 1990
A1:Title: Nucleotide sequences and three-dimensional model
A1:Reference number: S09740; MUID:90262535; PMID:2111699

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-146 <HUG>

C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>

Query Match	77.8%	Score 477.5	DB 2	Length 146
Best Local Similarity	73.2%	Pred. No. 9.3e-36		
Matches 90; Conservative	13;	Mismatches 9;	Indels 11;	Gaps 2

QY 2 ESGPGIVKPSQTLSLTCTVSGSIRSCGYWMSWRQPCKGKLEWIGNIYHSGNTYYNPSL 61
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 25 ESGPGLVKPSTLSLTCTSVSGGSVSSGGIYMGNWRQPPCKGLEWIGSIIFYSGSTYYNPSL 84

Page 2

QY 113 SS 114

C.date: 22-Nov-1993 #assembly revision 12-Apr-1996 #text change 20-Jun-2000

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OM protein - protein search, using sw model

Run on: February 10, 2004, 17:48:48 ; Search time 6.39091 Seconds
(without alignments)
838.855 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614
Sequence: 1 ESEGGVLVPSQTLSTLCTV.....RSDGVTLDNMGQGLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	440.5	71.7	129	1	HV2F_HUMAN
2	417	67.9	146	1	HV2I_HUMAN
3	381.5	62.1	117	1	HV2G_HUMAN
4	363.5	59.2	137	1	HV46_MOUSE
5	352.5	57.4	144	1	HV43_MOUSE
6	347.5	56.6	113	1	HV47_MOUSE
7	338.5	55.1	116	1	HV61_MOUSE
8	335	54.6	117	1	HV62_MOUSE
9	332.5	54.2	116	1	HV60_MOUSE
10	325	52.9	135	1	HV02_XENLA
11	314	51.1	120	1	HV2B_HUMAN
12	295.5	48.1	119	1	HV2C_HUMAN
13	294	47.9	147	1	HV2H_HUMAN
14	288.5	47.0	136	1	HV01_XENLA
15	288	46.9	115	1	HV44_MOUSE
16	288	46.9	119	1	HV40_MOUSE
17	287.5	46.8	125	1	HV42_HUMAN
18	286.5	46.7	121	1	HV2E_HUMAN
19	285.5	46.5	117	1	HV2B_RABIT
20	283	46.1	126	1	HV2A_HUMAN
21	282	45.9	114	1	HV3B_HUMAN
22	281	45.8	122	1	HV3A_HUMAN
23	281	45.8	122	1	HV3G_HUMAN
24	278	45.3	119	1	HV37_MOUSE
25	277	45.1	116	1	HV05_CARAU
26	276.5	45.0	121	1	HV3J_HUMAN
27	276	45.0	119	1	HV38_MOUSE
28	275	44.8	116	1	HV45_MOUSE
29	274.5	44.7	142	1	HV01_XAT
30	274	44.6	136	1	HV2C_RABIT
31	273.5	44.5	117	1	HV41_MOUSE
32	273.5	44.5	117	1	HV42_MOUSE
33	272	44.3	114	1	HV2A_RABIT

34	271	44.1	122	1	HV3H_HUMAN	P01769 homo sapien
35	267	43.5	118	1	HV51_MOUSE	P06330 mus musculus
36	267	43.5	139	1	HV07_MOUSE	P01751 mus musculus
37	265.5	43.2	117	1	HV12_MOUSE	P01756 mus musculus
38	264.5	43.1	117	1	HV3D_HUMAN	P01765 homo sapien
39	264.5	43.1	115	1	HV13_MOUSE	P01757 mus musculus
40	264	43.0	122	1	HV20_MOUSE	P01789 mus musculus
41	262.5	42.8	115	1	HV3F_HUMAN	P01767 homo sapien
42	262.5	42.8	117	1	HV02_CANPA	P01785 canis famill
43	261	42.5	116	1	HV3T_HUMAN	P01781 homo sapien
44	261	42.5	126	1	HV3K_HUMAN	P01772 homo sapien
45	260	42.3	120	1	HV50_MOUSE	P06329 mus musculus

ALIGNMENTS

Query	Match	Score	DB	Length
2	ESGGVLVPSQTLSTLCTVSGSIRSGGYSWVRQPGKGLIEMIGNIYHSGNTYNSL	61		
6	ESGGVLVPSQTLSTLCTVSGSIRSGGYSWVRQPGKGLIEMIGNIYHSGNTYNSL	65		
62	KSRITMSVDSKKNFSLRLSVTAADTAIVYCAR	108		
66	RGRVTISVDSRNPFSNLRSMASADTAMYYCAGNPPEYDITGSDG--IDWGGGT	123		
109	LVTVSS 114			
124	TVHVS 129			

RESULT 2

HV21 HUMAN STANDARD; PRT; 146 AA.
 ID HV21 HUMAN
 AC P06331;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II region ARH-77 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85205332; PubMed=3922855;
 RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
 RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
 RT repeat sequence in 5' flanking region.";
 RL Gene 33:181-189 (1985).
 DR PIR; A02101; GIHUR2.
 DR HSSP; P01825; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT CHAIN 1 19
 FT DOMAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.
 FT DOMAIN 20 117 V SEGMENT.
 FT DOMAIN 118 127 D SEGMENT.
 FT DOMAIN 128 146 J SEGMENT.
 FT DISULFID 42 115 BY SIMILARITY.
 FT NON_TER 146 146
 SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218117F CRC64;

Query Match 67.9%; Score 417; DB 1; Length 146;
 Best Local Similarity 68.6%; Pred. No. 6.2e-36;
 Matches 83; Conservative 10; Mismatches 16; Indels 12; Gaps 3;

QY 4 GPELVKPSQTLSTLCVSGSGSIRSGYMSWRQPEPKGLEWIGNIYHSNTYNSPLK 63
 DB 28 GAGLVKPSQTLSTLCVSGSGSIRSGYMSWRQPEPKGLEWIGNIYHSNTYNSPLK 85
 QY 64 RIMTSVDTSKNHFSLRITSVTADTAAYYCARG--DG-----YTLDNWGCGTLVTVSS 113
 DB 86 RRVTLVDTSKNHFSLRITSVTADTAAYYCARGLKGMDVDYRGMDVWGCGTLVTVSS 145
 QY 114 S 114
 DB 146 S 146

RESULT 3
 HV2G HUMAN STANDARD; PRT; 117 AA.
 ID HV2G HUMAN
 AC P01825;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region NEMM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77242302; PubMed=407927;
 RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;

RT "Amino acid sequence of the VH region of a human myeloma
 RT immunoglobulin (Ig New)."
 RL Biochemistry 16:3412-3420 (1977).
 RN [2]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
 RX MEDLINE=78066916; PubMed=618887;
 RA Saul F.A., Amzel L.M., Poljak R.J.;
 RT "Preliminary refinement and structural analysis of the Fab fragment
 RT from human immunoglobulin new at 2.0-A resolution."
 RL J. Biol. Chem. 253:585-597 (1978).
 CC -1 MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGGL MYELOMA
 CC PROTEIN.

CC -1 SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A90404; GIHUM.
 DR PDB; 7FAB; 31-JAN-94.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 111
 FT MOD_RES 1 111
 FT STRAND 3 7
 FT STRAND 11 12
 FT STRAND 14 15
 FT STRAND 18 25
 FT STRAND 30 31
 FT STRAND 33 39
 FT STRAND 41 42
 FT STRAND 46 51
 FT STRAND 53 54
 FT STRAND 57 59
 FT HELIX 61 63
 FT TURN 64 66
 FT STRAND 67 72
 FT TURN 73 76
 FT STRAND 77 82
 FT HELIX 87 89
 FT STRAND 91 98
 FT STRAND 104 107
 FT STRAND 111 115
 FT NON_TER 117 117

Query Match 62.1%; Score 381.5; DB 1; Length 117;
 Best Local Similarity 65.8%; Pred. No. 2.2e-32;
 Matches 75; Conservative 17; Mismatches 19; Indels 3; Gaps 2;

QY 2 ESGPGLVPSQTLSTLCVSGSGSIRSGYMSWRQPEPKGLEWIGNIYHSNTYNSPL 61
 DB 6 QSGPGLVPSQTLSTLCVSGSGSIRSGYMSWRQPEPKGLEWIGNIYHSNTYNSPL 63
 QY 62 KSRITMSVDTSKNHFSLRITSVTADTAAYYCARG--DGTYTLDNWGCGTLVTVSS 114
 DB 64 RRVTLVDTSKNHFSLRITSVTADTAAYYCARGLKGMDVDYRGMDVWGCGTLVTVSS 117

RESULT 4
 HV46 MOUSE STANDARD; PRT; 137 AA.
 ID HV46 MOUSE
 AC P01822;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig heavy chain V region MOPC 315 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A. PubMed=2497341;
 MEDLINE=89238351; Dorrington K.J., Klein M.;
 Riffert A., Horne C., Dorrington K.J., Klein M.;
 "Cloning, sequencing and expression of the rearranged MOPC 315 VH
 gene segment";
 Mol. Immunol. 26:431-434 (1989).
 [2]
 SEQUENCE OF 1-31.
 MEDLINE=78094475; PubMed=414225;
 Jilka R.L., Pestka S.;
 "Amino acid sequence of the precursor region of MOPC-315 mouse
 immunoglobulin heavy chain";
 Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).
 [3]
 SEQUENCE OF 1-21.
 MEDLINE=79148758; PubMed=428562;
 Schechter I., Wolf O., Zemell R., Burstein Y.;
 "Structure and function of immunoglobulin genes and precursors";
 Fed. Proc. 38:1839-1845 (1979).
 [4]
 SEQUENCE OF 19-136.
 MEDLINE=74170779; PubMed=4524622;
 Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
 "Amino-acid sequence of the variable region of the heavy (alpha)
 chain of a mouse myeloma protein with anti-hapten activity";
 Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127 (1974).
 [5]
 REVISION TO 53.
 MEDLINE=77244979; PubMed=268248;
 Hood L., Margolies M.N., Givol D., Zakut R.;
 Unpublished results, cited by:
 Padlan E.A., Davies D.R., Peck I., Givol D., Wright C.;
 Cold Spring Harb. Symp. Quant. Biol. 41:627-637 (1977).
 -I- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
 PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.

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 CC EMBL: M27638; AAA61337.1; -
 CC EMBL: X07880; CAA30727.1; -
 CC PIR: P0102; AYMS35.
 DR HSP: P01825; 7FAB.
 DR InterPro: IPR007110; IG-1like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 137 IG HEAVY CHAIN V REGION MOPC 315.
 FT DOMAIN 19 48 FRAMEWORK-1.
 FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 85 116 FRAMEWORK-3.
 FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 127 137 FRAMEWORK-4.
 FT DISULFID 40 114 BY SIMILARITY.
 FT CONFLICT 15 15 G-> GG (IN REF. 1; CAA30727).
 FT CONFLICT 15 15 G-> H (IN REF. 2).
 FT CONFLICT 77 78 GY-> YG (IN REF. 4).
 FT CONFLICT 102 102 N-> D (IN REF. 4).
 FT CONFLICT 123 123 MISSING (IN REF. 4).
 FT NON_TER 137 137

SEQUENCE 137 AA; 15399 MW; FB828304C2B81DC CRC64;
 Query Match 59.2%; Score 363.5; DB 1; Length 137;
 Best Local Similarity 60.9%; Pred. No. 1.8e-30;
 Matches 70; Conservative 18; Mismatches 24; Indels 3; Gaps 2;
 Oy 2 ESGPGLVPSQTLTCTVSGSIRSGGYWVROPKGLEWIGNIGNTYNSL 61
 Db 24 ESGPGLVPSQTLTCTVSGSIRSGGYWVROPKGLEWIGNIGNTYNSL 82
 Oy 62 KSRTMSVDTSKNHFSLRTSVTAADPAVYCAASDC--YTLDMWGQTLTVSS 114
 Db 83 KNRVSITRDTSNQFLKINSVTTEDPATYTCAGDNHLYFYFDWGGQTLTVSS 137
 RESULT 5
 ID HV43 MOUSE STANDARD; PRT; 144 AA.
 AC P01819;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MOPC 141 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A. PubMed=6774258;
 RX MEDLINE=81012133; PubMed=6774258;
 RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
 "Two types of somatic recombination are necessary for the generation
 of complete immunoglobulin heavy-chain genes";
 Nature 286:676-683 (1980).
 CC -I- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
 CC DIFFERENTIAL GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

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 CC EMBL: V00768; CAA24149.1; -
 CC PIR: A02094; G2MS14.
 DR HSP: P01825; 7FAB.
 DR InterPro: IPR007110; IG-1like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.
 FT DOMAIN 20 130 IG-LIKE.
 FT NON_TER 144 144
 SQ SEQUENCE 144 AA; 15759 MW; 8E47ACB3706D30A CRC64;
 Query Match 57.4%; Score 352.5; DB 1; Length 144;
 Best Local Similarity 59.8%; Pred. No. 2.6e-29;
 Matches 73; Conservative 16; Mismatches 22; Indels 11; Gaps 3;
 Oy 2 ESGPGLVPSQTLTCTVSGSIRSGGYWVROPKGLEWIGNIGNTYNSL 61
 Db 25 ESGPGLVPSQTLTCTVSGSIRSGGYWVROPKGLEWIGNIGNTYNSL 82
 Oy 62 KSRTMSVDTSKNHFSLRTSVTAADPAVYCA-----RSDGY-TLDMWGQTLTV 112
 Db 83 KSRLLITDNRKSGVFLKMSLQTDITARYYCAASIVYGRSDKYLFLDWMGGQTSYTV 142

QY 113 SS 114
 Db 143 SS 144

RESULT 6

HV47_MOUSE STANDARD; PRT; 113 AA.
 AC P01823;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 36-60.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIRSONATE
 MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND
 IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIRSONATE RESPONSE OF
 STRAIN A/J MICE.
 CC PIR; A02098; GMS60.
 DR PDB; 1J10; 18-FEB-03.
 DR PDB; 1J1X; 18-FEB-03.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; 3D-structure.
 FT NON TER 113
 SQ SEQUENCE 113 AA; 12734 MW; 38DC0E0B3F507B7 CRC64;

Query Match 56.6%; Score 347.5; DB 1; Length 113;
 Best Local Similarity 61.9%; Pred. No. 6.4e-29;
 Matches 70; Conservative 15; Mismatches 23; Indels 5; Gaps 2;

QY 2 ESGPGLVPSQSLTCTCTVSGSGSIRSGGYVSWVRQPPGKGLVIGTINIHSGNTYNNPSL 61
 |||||
 Db 6 ESGPGLVPSQSLTCTCTVSGSGSIRSGGYVSWVRQPPGKGLVIGTINIHSGNTYNNPSL 63
 |||||
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSDGYTLDMNGGTLVTVSS 114
 |||||
 Db 64 KSRITSDTDSKNQYFLQNLNSVTSEDTATYTC---SLRPAYGGGTLVTVSA 113
 |||||

RESULT 7

HV61_MOUSE STANDARD; PRT; 116 AA.
 AC P18532;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 1843 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;

RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response."
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
 DR PIR; J0508; HVM51B.
 DR PDB; 1KCS; 11-MAY-02.
 DR PDB; 1KCV; 11-MAY-02.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal; 3D-structure.

FT SIGNAL 1 18 IG HEAVY CHAIN V REGION 1843.
 FT CHAIN 19 116 FRAMEWORK-1.
 FT DOMAIN 19 48 FRAMEWORK-1.
 FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 54 67 FRAMEWORK-2.
 FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 85 116 FRAMEWORK-3.
 FT DISULFID 40 114 BY SIMILARITY.
 FT NON TER 116
 SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681PF74 CRC64;

Query Match 55.1%; Score 338.5; DB 1; Length 116;
 Best Local Similarity 70.2%; Pred. No. 5.5e-28;
 Matches 66; Conservative 10; Mismatches 17; Indels 1; Gaps 1;

QY 2 ESGPGLVPSQSLTCTCTVSGSGSIRSGGYVSWVRQPPGKGLVIGTINIHSGNTYNNPSL 61
 |||||
 Db 24 ESGPGLVPSQSLTCTCTVSGSGSIRSGGYVSWVRQPPGKGLVIGTINIHSGNTYNNPSL 82
 |||||
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCAR 95
 |||||
 Db 83 KSRITSDTDSKNQYFLQNLNSVTSEDTATYTCAR 116
 |||||

RESULT 8

HV62_MOUSE STANDARD; PRT; 117 AA.
 AC P18533;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 733 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE=89279149; PubMed=2499654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response."
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; J0510; HVM573.
 DR HSSP; P01825; 7EAB.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 18 IG HEAVY CHAIN V REGION 733.
 FT CHAIN 19 117
 FT DOMAIN 19 >117 IG-LIKE.

```

FT DISULFID 40 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13223 MW; 159551782F976BE CRC64;

Query Match
Best Local Similarity 54.6%; Score 335; DB 1; Length 117;
Matches 63; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 2 ESGPGLVPSQTLSTCTVSGSISGSGYMSWROPKGLKLEWIGNTYHSGNTYYNSL 61
DB 24 ESGPGLVPSQTLSTCTVSGSISGSGYMSWROPKGLKLEWIGNTYHSGNTYYNSP 83
QY 62 KSRTMSVDTSKNHFSLRLTSTVTAADTAVYYCAR 95
DB 84 KSRTITRDTSKNOFLEWNSLTAEADTAVYYCAR 117

RESULT 9
HV60 MOUSE STANDARD; PRT; 116 AA.
AC P18531.
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region M315 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/CJ.
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
DR PIR_UT0509; HVM51.
DR HSSP_P01825; 7FAB.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION M315.
FT DOMAIN 19 48 FRAMWORK-1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 67 FRAMWORK-2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMWORK-3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON TER 116 116
SQ SEQUENCE 116 AA; 13095 MW; 4562E03E53DC9E10 CRC64;

Query Match
Best Local Similarity 54.2%; Score 332.5; DB 1; Length 116;
Matches 63; Conservative 13; Mismatches 17; Indels 1; Gaps 1;

QY 2 ESGPGLVPSQTLSTCTVSGSISGSGYMSWROPKGLKLEWIGNTYHSGNTYYNSL 61
DB 24 ESGPGLVPSQTLSTCTVSGSISGSGYMSWROPKGLKLEWIGNTYHSGNTYYNSL 82
QY 62 KSRTMSVDTSKNHFSLRLTSTVTAADTAVYYCAR 95
DB 83 KSRTITRDTSKNOFLEWNSLTAEADTAVYYCAR 116

RESULT 10
HV02 XENLA STANDARD; PRT; 135 AA.
ID HV02_XENLA

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AC P20957;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region XIG14 precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis Igm deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains."
RT Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC -1-SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; J03632; AAA9791.1; -.
DR PIR; B31933; B31933.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR KW Immunoglobulin V region; Signal.
FT NON TER 1 1
FT SIGNAL 1 18
FT CHAIN 19 135 IG HEAVY CHAIN V REGION XIG14.
FT DOMAIN 19 128 IG-LIKE.
FT DOMAIN 135 135
FT NON TER 135 135
SQ SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Query Match
Best Local Similarity 52.9%; Score 325; DB 1; Length 135;
Matches 63; Conservative 17; Mismatches 31; Indels 4; Gaps 2;

QY 2 ESGPGLVPSQTLSTCTVSGSISGSGYMSWROPKGLKLEWIGNTYHSGNTYYNSL 61
DB 23 ESGPGLVPSQTLSTCTVSGSISGSGYMSWROPKGLKLEWIGNTYHSGNTYYNSL 80
QY 62 KSRTMSVDTSKNHFSLRLTSTVTAADTAVYYCAR--SDGYTLDMWGQGLTVTVSS 114
DB 81 KSRTITRDTSKNOFLEWNSLTAEADTAVYYCAR--SDGYTLDMWGQGLTVTVSS 135

RESULT 11
HV2B HUMAN STANDARD; PRT; 120 AA.
ID HV2B_HUMAN
AC P01815.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region COR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;

```

RA Prese E.M., Hogg N.M.;
 RT "The amino acid sequences of the Fd fragments of two human gamma-1
 heavy chains";
 RL Biochem. J. 117:641-660(1970).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CC PROTEIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR: A02089; G1HUCO.
 DR HSSP; P01825; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KM Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.
 FT MOD RES 1 110
 FT DISULFID 22 94
 FT CARBOHYD 62 62
 FT NON TER 120 120
 SQ SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EEB98 CRC64;
 Query Match 51.1%; Score 314; DB 1; Length 120;
 Best Local Similarity 55.5%; Pred. No. 1,9e-25;
 Matches 66; Conservative 14; Mismatches 29; Indels 10; Gaps 3;
 QY 2 EESGPGVLRPSQTLSTLCVSGSIRSGGYMSWVROPKGLGEMIGNIYHSNTYYNPSL 61
 DB 6 EESGPAVLRPTQTLTLCTFSGFSLSGTCMVCWMIKQPGKGLMLARIDMDDKYIGSL 65
 DB 66 ETRLTISKDTSKNQVVLTMPPV---DTATYCARITVTPAPAGY-MDVWGRTPTVSS 120
 QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAVYYCAR-----SDGYTLDMNGQGLTVSS 114
 DB 66 ETRLTISKDTSKNQVVLTMPPV---DTATYCARITVTPAPAGY-MDVWGRTPTVSS 120
 RESULT 12
 ID HV2H HUMAN STANDARD; PRT; 119 AA.
 AC P01816;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-II region DM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=70258837; PubMed=5449120;
 RA Prese E.M., Hogg N.M.;
 RT "The amino acid sequences of the Fd fragments of two human gamma-1
 heavy chains";
 RL Biochem. J. 117:641-660(1970).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE
 CC SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR: A02091; G1HUP.
 DR HSSP; P01789; 1MCP.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KM Immunoglobulin V region; Pyrrolidone carboxylic acid.

FT DOMAIN 1 113 IG-LIKE.
 FT MOD RES 1 1
 FT NON TER 119 119
 SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;
 Query Match 48.1%; Score 295.5; DB 1; Length 119;
 Best Local Similarity 52.6%; Pred. No. 1,5e-23;
 Matches 60; Conservative 16; Mismatches 37; Indels 1; Gaps 1;
 QY 2 EESGPGVLRPSQTLSTLCVSGSIRSGGYMSWVROPKGLGEMIGNIYHSNTYYNPSL 61
 DB 6 EESGPAVLRPTQTLTLCTFSGFSLSGTCMVCWMIKQPGKGLMLARIDMDDKYIGSL 65
 DB 66 ETRLTISKDTSKNQVVLTMPPV---DTATYCARITVTPAPAGY-MDVWGRTPTVSS 119
 QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAVYYCARSDG-YTLDMNGQGLTVSS 114
 DB 66 ETRLTISKDTSKNQVVLTMPPV---DTATYCARITVTPAPAGY-MDVWGRTPTVSS 119
 RESULT 13
 ID HV2H HUMAN STANDARD; PRT; 147 AA.
 AC P04438;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V-II region SSS precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84298107; PubMed=6089186;
 RA Takahashi N., Noma T., Honjo T.;
 RT "Rearranged immunoglobulin heavy chain variable region (VH)
 pseudogene that deletes the second complementarity-determining
 region";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5194-5198(1984).
 DR PIR; A02090; G2HUCS.
 DR HSSP; P01825; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KM Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 147 IG HEAVY CHAIN V-II REGION SSSS.
 FT DOMAIN 20 118 V SEGMENT.
 FT DOMAIN 119 132 D SEGMENT.
 FT DOMAIN 133 147 J SEGMENT.
 FT NON TER 147 147
 SQ SEQUENCE 147 AA; 16323 MW; FCBDB3D00FB666 CRC64;
 Query Match 47.9%; Score 294; DB 1; Length 147;
 Best Local Similarity 49.6%; Pred. No. 2,7e-23;
 Matches 58; Conservative 15; Mismatches 34; Indels 10; Gaps 1;
 QY 2 EESGPGVLRPSQTLSTLCVSGSIRSGGYMSWVROPKGLGEMIGNIYHSNTYYNPSL 61
 DB 25 EESGPAVLRPTQTLTLCTFSGFSLSGTCMVCWMIKQPGKGLMLARIDMDDKYIGSL 84
 QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAVYYCARSDG-----GYTLDMNGQGLTVSS 108
 DB 85 ETRLTISKDTSKNQVVLTMPPV---DTATYCARITVTPAPAGY-MDVWGRTPTVSS 141
 RESULT 14
 ID HV01 XENLA

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ID HV01_XENLA STANDARD; PRT; 136 AA.
AC P20956;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region XIG8 precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Fipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=83355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis Igm deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains."
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL: M20484; AAA49774.1; ALT_TERM.
CC PIR: A31933; A31933.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19 136 IG HEAVY CHAIN V REGION XIG8.
FT DOMAIN 19 128 IG-LIKE.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15123 MW; 3141838981441963 CRC64;

Query Match 47.0%; Score 288.5; DB 1; Length 136;
Best Local Similarity 50.4%; Pred. No. 9e-23;
Matches 59; Conservative 19; Mismatches 32; Indels 7; Gaps 3;

QY 2 ESGPGLVRSQTLSTCTVSGSIRSGGYMSWVROPFGKLEWIGNIYHSGNTYYPBL 61
DB 23 ESGPGLVRSQTLSTCTVSGSIRSGGYMSWVROPFGKLEWIGNIYHSGNTYYPBL 80
QY 62 KSRITMSVDTSKNHSRLTSTVTAADTARYYC-----ARSDGTTLDNMGCGTLVTVSS 114
DB 81 KNRVTITKDKGKQVYLTQNNGMEVVDXTAMYCTSTLAGAGY-FEHMGQITVTVTS 136

RESULT 15
HV44_MOUSE STANDARD; PRT; 115 AA.
ID HV44_MOUSE
AC P01820;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region PJ14 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes."
RL Nature 286:676-683(1980).
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL: V00767; CAA24148.1; -.
CC PIR: A02095; HVMS14.
DR PDB; 1A7N; 29-APR-98.
DR PDB; 1A7O; 29-APR-98.
DR PDB; 1A7P; 29-APR-98.
DR PDB; 1A7R; 29-APR-98.
DR PDB; 1G7H; 17-JAN-01.
DR PDB; 1G7I; 17-JAN-01.
DR PDB; 1G7J; 17-JAN-01.
DR PDB; 1G7M; 17-JAN-01.
DR PDB; 43C9; 24-JUL-02.
DR PDB; 43CA; 24-JUL-02.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1
FT CHAIN 20 115 IG HEAVY CHAIN V REGION PJ14.
FT DOMAIN 20 >115 IG-LIKE.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12447 MW; 7569DD4A4843D500 CRC64;

Query Match 46.9%; Score 288; DB 1; Length 115;
Best Local Similarity 60.2%; Pred. No. 8.4e-23;
Matches 56; Conservative 15; Mismatches 20; Indels 2; Gaps 1;

QY 2 ESGPGLVRSQTLSTCTVSGSIRSGGYMSWVROPFGKLEWIGNIYHSGNTYYPBL 61
DB 25 ESGPGLVRSQTLSTCTVSGSIRSGGYMSWVROPFGKLEWIGNIYHSGNTYYPBL 82
QY 62 KSRITMSVDTSKNHSRLTSTVTAADTARYYCA 94
DB 83 KSRITMSVDTSKNHSRLTSTVTAADTARYYCA 115

Search completed: February 10, 2004, 18:36:30
Job time : 7.39091 secs

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Query No.	Score	Match Length	DB	ID	Description
1	466	75.9	150	4	Q95973
2	466	75.9	456	4	Q96KX8
3	463.5	75.5	119	4	Q9UL73
4	457	74.4	613	4	Q96EY0
5	429	69.9	130	4	Q812D7
6	426.5	69.5	588	4	Q8WUX4
7	426.5	69.5	597	4	Q9BU10
8	426.5	69.5	618	4	Q96AA5
9	422.5	68.8	557	4	Q9BD88
10	413	67.3	473	4	Q8TC63
11	382.5	62.3	479	11	Q9SM22
12	365	59.4	122	4	Q9UL76
13	346.5	56.4	121	4	Q9UL95
14	339	55.2	111	11	Q99NG4
15	335	54.6	482	11	Q91X92
16	315.5	51.4	118	4	Q9UL74

17	237.5	48.5	493	4	Q8NCU6	Q8ncf6 homo sapien
18	294	47.9	613	4	Q8MUK1	Q8mkt1 homo sapien
19	293.5	47.8	116	4	Q9UL93	Q9ul93 homo sapien
20	232.5	47.6	597	4	Q96BB9	Q96bb9 homo sapien
21	291	47.4	147	4	Q9Y509	Q9y509 homo sapien
22	290	47.2	484	11	Q8V8A0	Q8v8a0 mus muscul
23	289	47.1	118	4	Q9UL72	Q9ul72 homo sapien
24	286.5	46.7	113	4	Q9UL90	Q9ul90 homo sapien
25	282	45.9	145	11	Q924P7	Q924p7 mus muscul
26	282	45.9	145	11	Q924R1	Q924r1 mus muscul
27	281	45.8	145	11	Q924R4	Q924r4 mus muscul
28	280	45.6	471	4	Q8TC77	Q8tc77 homo sapien
29	279.5	45.5	117	11	Q9QX99	Q9qxe9 mus muscul
30	279.5	45.5	121	4	Q9UL71	Q9ul71 homo sapien
31	279.5	45.5	481	11	Q91W11	Q91wt1 mus muscul
32	279.5	45.5	486	11	Q91Z07	Q91z07 mus muscul
33	279.5	45.5	499	4	Q8NSK4	Q8nsk4 homo sapien
34	279	45.4	494	4	Q96K68	Q96k68 homo sapien
35	278.5	45.4	142	11	Q924O1	Q924o1 mus muscul
36	278	45.3	298	11	Q92QY0	Q92qf0 mus muscul
37	277	45.1	118	4	Q9UL91	Q9ul91 homo sapien
38	276.5	45.0	117	11	Q9QX00	Q9qxf0 mus muscul
39	275.5	44.9	119	5	Q9GYZ2	Q9gyz2 schistosoma
40	275.5	44.9	480	11	Q91X11	Q91xel mus muscul
41	275	44.8	112	4	Q9HC11	Q9hct1 homo sapien
42	275	44.8	122	4	Q9UL84	Q9ul84 homo sapien
43	275	44.8	143	11	Q924R0	Q924r0 mus muscul
44	275	44.8	469	11	Q8R3V9	Q8rtv9 mus muscul
45	275	44.8	573	4	Q8WU38	Q8wu38 homo sapien

ALIGNMENTS

RESULT 1
095973

ID 095973 PRELIMINARY; PRT; 150 AA.

AC 095973; 10 (2004-3)

DT	01-MAY-1999 (TTFMBI.re)	10	Last sequence update)
DI	01-MAY-1999 (ITEMBL.re)	10	Created)

DT 01-MAR-2003 (Tremblay, 23, last annotation update)

DE VH4 heavy chain variable region precursor (Fragment)

GN	IGM.

05 Homo sapiens (Human) .

OC Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Hominidae: Homo

NCBI TaxID=9606;

$$\mathbf{R}^N \quad [1] \quad -$$

RP SEQUENCE FROM N.

RA Sun C.-H., Song C.-H., Lee S.-K.;
[C] proliferation of TCM secreting B cell] in the environment of

Behcet's patient with arthritis.":
 clonal proliferation of lymphocytes in the synovium of

Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF103795; AAC79084.1; -.

DR HSSP; P01825; 7FAB.

DR InterPro: IPR001110; Ig-like-
DR InterPro: IPR003006; Ig MHC

InterPro: IPR003596; 1q V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; IG_LIKE; 1.

ET	1	19
kw		
SIGNAL		

FT	CHAIN	20	>150
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FT	NON TER	150	150
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SQ	SEQUENCE	150 AA;	16315 MW;
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Myer Match 75.98:

Best Local Similarity 76.18;

Matches 86; Conservative 12

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2 ES G P G L V K P S Q I L S L I C I V S

Db 25 ESGPGLVPSKPSLSTCTVSGSGSSSTNYWGMIRQPEKGLGEMISLHNSGSDYNNPSL 84
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSGYTLDMNGGTLTVSS 114
 DB 85 KSRVITISVDTSKNQPSLRLSTVTAADTAAYVYCARLGMGAFDFGHTMTVSS 137

RESULT 2

Q96KX8 PRELIMINARY; PRT; 496 AA.

AC Q96KX8; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN NCBI_Taxid=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC016369; AAH16369.1; -
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 75.9%; Score 466; DB 4; Length 496;
 Best Local Similarity 74.2%; Pred. No. 1.2e-40;
 Matches 89; Conservative 10; Mismatches 13; Indels 8; Gaps 2;

QY 2 ESGPGLVPSKPSLSTCTVSGSGSIRSGGYWVWVQPPGKGLGEMIGNIYHSGNTYNNPSL 61
 DB 25 ESGPGLVPSKPSLSTCTVSGSGSIRSGGYWVWVQPPGKGLGEMIGNIYHSGNTYNNPSL 84
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSGDYTLDMNGGTLTVSS 114
 DB 85 KSRVITISVDTSKNQPSLRLSTVTAADTAAYVYCAR-HGYSKSGRTGALDIWGGTLTVSS 143

RESULT 3

Q9UL73 PRELIMINARY; PRT; 119 AA.

AC Q9UL73; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN NCBI_Taxid=9606;
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M., Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
 CL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035041; AAD56277.1; -
 DR HSP; P01825; 7PAB.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 119
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EA0BE CRC64;

Query Match 75.5%; Score 463.5; DB 4; Length 119;
 Best Local Similarity 77.6%; Pred. No. 3.8e-41;
 Matches 90; Conservative 9; Mismatches 12; Indels 5; Gaps 2;

QY 2 ESGPGLVPSKPSLSTCTVSGSGSIRSGGYWVWVQPPGKGLGEMIGNIYHSGNTYNNPSL 61
 DB 6 ESGPGLVPSKPSLSTCTVSGSGSIRSGGYWVWVQPPGKGLGEMIGNIYHSGNTYNNPSL 63
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSGDYTLDMNGGTLTVSS 114
 DB 64 KSRVITISVDTSKNQPSLRLSTVTAADTAAYVYCARLGMGAFDFGHTMTVSS 119

RESULT 4

Q96EY0 PRELIMINARY; PRT; 613 AA.

AC Q96EY0; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN NCBI_Taxid=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011857; AAH11857.1; -
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IGV; 5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 74.4%; Score 457; DB 4; Length 613;
 Best Local Similarity 78.0%; Pred. No. 1.4e-39;
 Matches 92; Conservative 7; Mismatches 11; Indels 8; Gaps 3;

QY 2 ESGPGLVPSKPSLSTCTVSGSGSIRSGGYWVWVQPPGKGLGEMIGNIYHSGNTYNNPSL 61
 DB 25 ESGPGLVPSKPSLSTCTVSGSGSIRSGGYWVWVQPPGKGLGEMIGNIYHSGNTYNNPSL 82
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSGDYTLDMNGGTLTVSS 114
 DB 83 KSRVITISVDTSKNQPSLRLSTVTAADTAAYVYCAR-SQPWELPTVGLFYWGQTLTVSS 139

RESULT 5

Q81ZD7 PRELIMINARY; PRT; 130 AA.

AC Q81ZD7; 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Anti-thyroglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RA Jang Y.-J., Chung J., Park J.-Y.;
 RT "Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-
 RL Thymoglobulin Single Chain Fv from SLE Patient by Phage Display."
 DR Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY145445; AAN64329.1; --
 FT NON TER 1
 FT NON TER 130
 SQ SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;

Query Match 69.5%; Score 429; DB 4; Length 130;
 Best Local Similarity 68.8%; Pred. No. 1.8e-37;
 Matches 86; Conservative 12; Mismatches 15; Indels 12; Gaps 4;

OY 2 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWVWROPKGLWIGNIYHSGNT-----Y 56
 DB 6 QSGPGLVPSQTLSTCTVSGGSIIRSGGYWVWROPKGLWIGNIYHSGNTYSGSPY 65
 OY 57 YNPSLKSRIITMSVDTSKNHFSLRLSVTAADTAAYYCAR-----SDG--YT-LDNWGQGL 109
 DB 66 YAPSLRSRVIIISVDTSKQSLSLKSSVNAADTAAYYCARPTHCSCGCGYAFQHWGQGL 125
 OY 110 VTWSS 114
 DB 126 VTWSS 130

RESULT 6

OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC019235; AAH19235.1; --
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 5.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 5.
 DR PROSITE: PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;

AC 08WUX4 PRELIMINARY; PRT; 588 AA.
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC019235; AAH19235.1; --
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 5.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 5.
 DR PROSITE: PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;

Query Match 69.5%; Score 426.5; DB 4; Length 588;
 Best Local Similarity 70.0%; Pred. No. 2.2e-36;
 Matches 84; Conservative 10; Mismatches 15; Indels 11; Gaps 3;

OY 4 GPGLVPSQTLSTCTVSGGSIIRSGGYWVWROPKGLWIGNIYHSGNTYHNSPLSKS 63
 DB 27 GAGLKPSETLSTCTGVYGSF--SGYWSVIRPPKGLWIGNIYHSGNTYHNSPLSKS 84
 OY 64 RTTMSVDTSKNHFSLRLSVTAADTAAYYCAR-----SDG--YT-LDNWGQGLVTWSS 114
 DB 85 RVTISVDTSKQSLSLKSSVNAADTAAYYCARVITRASPGTDGRYGMVWGQGLVTWSS 144

RESULT 7
 O9BU10 PRELIMINARY; PRT; 597 AA.

AC Q9BU10;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC002963; AAH02963.1; --
 DR HSPD, P01825; FRAB.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 5.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 5.
 DR PROSITE: PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8F87E055851 CRC64;

Query Match 69.5%; Score 426.5; DB 4; Length 597;
 Best Local Similarity 70.0%; Pred. No. 2.2e-36;
 Matches 84; Conservative 10; Mismatches 15; Indels 11; Gaps 3;

OY 4 GPGLVPSQTLSTCTVSGGSIIRSGGYWVWROPKGLWIGNIYHSGNTYHNSPLSKS 63
 DB 27 GAGLKPSETLSTCTGVYGSF--SGYWSVIRPPKGLWIGNIYHSGNTYHNSPLSKS 84
 OY 64 RTTMSVDTSKNHFSLRLSVTAADTAAYYCAR-----SDG--YT-LDNWGQGLVTWSS 114
 DB 85 RVTISVDTSKQSLSLKSSVNAADTAAYYCARVITRASPGTDGRYGMVWGQGLVTWSS 144

RESULT 8

OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC017356; AAH17356.1; --
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 5.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 5.
 DR PROSITE: PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;

Query Match 69.5%; Score 426.5; DB 4; Length 618;
 Best Local Similarity 70.0%; Pred. No. 2.3e-36;
 Matches 84; Conservative 10; Mismatches 15; Indels 11; Gaps 3;

OY 4 GPGLVPSQTLSTCTVSGGSIIRSGGYWVWROPKGLWIGNIYHSGNTYHNSPLSKS 63
 DB 27 GAGLKPSETLSTCTGVYGSF--SGYWSVIRPPKGLWIGNIYHSGNTYHNSPLSKS 84

DB 27 GAGLKPSETLSLTCGVGGSF--SGYWMIRQPPGKLEWIGELINHSNSTYNSLS 84
 QY 64 RITMSVDTSKNHSLSLTSTVADTAIVYTCAR-----SDG-YTLDMWGQTLVTSS 114
 DB 85 RVTISVDTSKKQLSLKLSVNAADTAIVYTCARVITRASPGTDGRYGMVDWGQTLVTSS 144

RESULT 9

Q9BOB8 PRELIMINARY; PRT; 597 AA.
 AC Q9BOB8; 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle, and Lymph;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006180; AAH06180.1; -
 DR EMBL; BC001872; AAH01872.1; -
 DR HSSP; P01825; 7FAB.
 DR InterPro; IPR007110; Ig-1like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 68.8%; Score 422.5; DB 4; Length 597;
 Best Local Similarity 70.0%; Pred. No. 5.8e-36;
 Matches 84; Conservative 9; Mismatches 16; Indels 11; Gaps 3;

QY 4 GPGVLKPSQTLSTCTVSGGSIKSGYWMVWQPPGKLEWIGELINHSNSTYNSLS 63
 DB 27 GAGLKPSETLSLTCGVGGSF--SGYWMIRQPPGKLEWIGELINHSNSTYNSLS 84
 QY 64 RITMSVDTSKNHSLSLTSTVADTAIVYTCAR-----SDG-YTLDMWGQTLVTSS 114
 DB 85 RVTISVDTSKKQLSLKLSVNAADTAIVYTCARVITRASPGTDGRYGMVDWGQTLVTSS 144

RESULT 10

Q8TC63 PRELIMINARY; PRT; 473 AA.
 AC Q8TC63; 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025885; AAH25885.1; -
 DR InterPro; IPR000923; BlueCu_1.
 DR InterPro; IPR007110; Ig-1like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 4.

DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00196; COPPER BLUE; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 67.3%; Score 413; DB 4; Length 473;

Best Local Similarity 69.0%; Pred. No. 4.4e-35;
 Matches 80; Conservative 11; Mismatches 15; Indels 6; Gaps 2;

QY 2 ESGPGLKPSQTLSTCTVSGGSIKSGYWMVWQPPGKLEWIGELINHSNSTYNSLS 61
 DB 32 ESGPGLKPSQTLSTCTVSGSVASSSYGMVWQPPGKLEWIGELINHSNSTYNSLS 91
 QY 62 KSRITMSVDTSKNHSLSLTSTVADTAIVYTCARBDGTL---DNMGQTLVTSS 113
 DB 92 RSRVTMSADMSNSFYLKIDSVTADTAIVYCA--GHLVWGFGAHWQGKLVSVS 145

RESULT 11

Q99M22 PRELIMINARY; PRT; 479 AA.
 AC Q99M22; 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical 52.0 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002091; AAH02091.1; -
 DR HSSP; P01810; 2FAB.
 DR InterPro; IPR007110; Ig-1like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;

Query Match 62.3%; Score 382.5; DB 11; Length 479;
 Best Local Similarity 66.7%; Pred. No. 7.2e-32;
 Matches 76; Conservative 15; Mismatches 20; Indels 3; Gaps 3;

QY 2 ESGPGLKPSQTLSTCTVSGGSIKSGYWMVWQPPGKLEWIGELINHSNSTYNSLS 61
 DB 24 ESGPGLKPSQTLSTCTVSGSVASSSYGMVWQPPGKLEWIGELINHSNSTYNSLS 82
 QY 62 KSRITMSVDTSKNHSLSLTSTVADTAIVYTCARBDGTL---DNMGQTLVTSS 114
 DB 83 KSRITMSVDTSKNHSLSLTSTVADTAIVYTCARBDGTL---DNMGQTLVTSS 135

RESULT 12

Q9UL75 PRELIMINARY; PRT; 122 AA.
 AC Q9UL75; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berner S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035039; AAD56275.1; -.
 DR HSSP; P01825; 7FAB.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON TER 1
 FT NON TER 122
 SQ SEQUENCE 122 AA; 13719 MW; 56CB0612586A6529 CRC64;

Query Match 59.4%; Score 365; DB 4; Length 122;
 Best Local Similarity 61.5%; Pred. No. 9.2e-31;
 Matches 72; Conservative 12; Mismatches 29; Indels 4; Gaps 2;

OY 2 ESGPGLVPSQTLSTCTVSGSGSIRSGYMSWRQPPKGLGEMIGNIYHSGNTY--YNP 59
 DB 6 QSGPGLVPSQTLSTCTVSGSGSIRSGYMSWRQPPKGLGEMIGNIYHSGNTY--YNP 59
 60 SLKRTMSVDTSKNHFSLRLTSTVTAADPAVYVCARSDGY--TLNMGCGTLVTVSS 114
 DB 66 SVKSTITNPTSKQPSLQINSVTPEDTAVYVCARDLELGGFDYMGCGTLVTVSS 122

RESULT 13
 OYUL96 PRELIMINARY; PRT; 121 AA.
 AC OYUL96;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berner S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035039; AAD56275.1; -.
 DR HSSP; P01825; 7FAB.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON TER 1
 FT NON TER 121
 SQ SEQUENCE 121 AA; 13695 MW; D582D450596BD035 CRC64;

Query Match 56.4%; Score 346.5; DB 4; Length 121;
 Best Local Similarity 58.6%; Pred. No. 8.1e-29;
 Matches 68; Conservative 13; Mismatches 32; Indels 3; Gaps 1;

OY 2 ESGPGLVPSQTLSTCTVSGSGSIRSGYMSWRQPPKGLGEMIGNIYHSGNTY--YNP 61
 DB 66 SVKSTITNPTSKQPSLQINSVTPEDTAVYVCARDLELGGFDYMGCGTLVTVSS 122

DB 6 ESGPGLVPSQTLSTCTVSGSGSIRSGYMSWRQPPKGLGEMIGNIYHSGNTY--YNP 65
 OY 62 KSRITMSVDTSKNHFSLRLTSTVTAADPAVYVCAR---SDGYTLNMGCGTLVTVSS 114
 DB 66 KSRITTKDTSKNQVDLTMTMDPMDTATVYCAHRKSGDGYFDYMGCGTLVTVSS 121

RESULT 14
 OY9NG4 PRELIMINARY; PRT; 121 AA.
 AC OY9NG4;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Single chain Fv (Fragment).
 OS Mus musculus (Mouse).
 OC Plasmid PHEN1.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=98169018; PubMed=9510199;
 RA Hantsch H., Frank R., Hennecke M., Baensch M., Sohne B., Arseniev L.,
 RT "Site-directed C3a-Receptor Antibodies from Phage Display Libraries";
 RL J. Immunol. 160:2947-2958(1998).
 DR EMBL; AJ222590; CAA10890.1; -.
 DR HSSP; P01825; 7FAB.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Plasmid.
 FT NON TER 1
 FT NON TER 121
 SQ SEQUENCE 121 AA; 13255 MW; D293E4EBC8C9D5B CRC64;

Query Match 55.2%; Score 339; DB 11; Length 121;
 Best Local Similarity 59.0%; Pred. No. 5e-28;
 Matches 69; Conservative 14; Mismatches 28; Indels 6; Gaps 2;

OY 2 ESGPGLVPSQTLSTCTVSGSGSIRSGYMSWRQPPKGLGEMIGNIYHSGNTY--YNP 61
 DB 6 ESGPGLVPSQTLSTCTVSGSGSIRSGYMSWRQPPKGLGEMIGNIYHSGNTY--YNP 61
 62 KSRITMSVDTSKNHFSLRLTSTVTAADPAVYVCARSDGY--TLNMGCGTLVTVSS 114
 DB 64 ISRLSISKNSKQVFLKLSLQEDTATVYCAHRYKRYANADYMGCGSIVTVSS 120

RESULT 15
 OY1X92 PRELIMINARY; PRT; 482 AA.
 AC OY1X92;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Unknown (Protein for MGC:18822).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Straube R.;
 RL EMBL; BC011181; AAH1181.1; -.
 DR InterPro; IPR007110; IG_1like.

DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_Y.
 DR Pfam: PF0047; IG_4.
 DR SMART: SM00406; IG_1.
 DR PROSITE: PSS0835; IG_LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; 2.
 SQ SEQUENCE 482 AA; 51865 MW; 312E01F9C1BC7F3C CRC64;

Query Match 54.6%; Score 335; DB 11; Length 482;
 Best Local Similarity 59.1%; Pred. No. 7.3e-27;
 Matches 68; Conservative 15; Mismatches 28; Indels 4; Gaps 2;

Qy	2	ESGPGIVKPSQTLSTCTVSGGSIKSGYWSVROPFGKLEWIGNIYHSGNTYVPSL	61
Db	25	ESGPDIVAPSQSLTCTVSGFALTS--YAIWVROPFGKLEWIGVITGCVTINYSAL	82
Qy	62	KSRITWSVDTSKNHFSRLTSVTAADTAVYYCARSDGY--TLDNMGQTLVTYSS	114
Db	83	KSRISTSKNSKSGQVFLKNNSLTNTDNTARYYCARSDNTEGAMDYWGQTSVTYSS	137

Search completed: February 10, 2004, 18:39:20
 Job time : 26.9455 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:26:58 ; Search time 11.7455 Seconds
(without alignments)
933.402 Million cell updates/sec

Title: US-10-027-725A-9

Sequence: 1 LBSGGLVKSQSLTCTV.....RSDGYTLDNMGQGLTVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*

1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501.5	81.7	135	2 S78051	Ig heavy chain pre
2	497.5	81.0	147	2 S13519	Ig heavy chain V r
3	492.5	80.2	140	2 I37782	Ig variable region
4	490	79.8	130	2 S30534	Ig heavy chain V r
5	488.5	79.6	116	2 S37456	Ig mu chain - huma
6	487.5	79.4	130	2 S31690	Ig heavy chain V r
7	480.5	78.3	121	2 S41113	Ig heavy chain - h
8	479.5	78.1	155	2 S31511	Ig heavy chain - h
9	477.5	77.8	146	2 S09710	Ig heavy chain V r
10	477.5	77.8	155	2 S31512	Ig heavy chain - h
11	473.5	77.1	146	2 S09711	Ig heavy chain V r
12	472.5	77.0	127	2 S19668	Ig heavy chain V r
13	472.5	77.0	128	2 S31514	Ig heavy chain - h
14	472	76.9	137	2 S31676	Ig heavy chain V r
15	469	76.4	99	2 S26803	Ig heavy chain V r
16	467.5	76.1	123	2 S30530	Ig heavy chain V r
17	467	76.1	99	2 S26801	Ig heavy chain V r
18	467	76.1	122	2 S69912	Ig V-D-J region (N
19	465	75.7	139	2 S31586	Ig heavy chain V r
20	464	75.6	99	2 S26802	Ig heavy chain V r
21	461	75.1	145	2 S78055	Ig heavy chain pre
22	460.5	75.0	109	2 PH1673	Ig heavy chain V r
23	459	74.8	110	2 S44110	Ig heavy chain V-D
24	458	74.6	139	2 A41287	Ig heavy chain pre
25	457	74.4	118	2 A26340	Ig heavy chain pre
26	454	73.9	97	2 PLO118	Ig heavy chain V-I
27	454	73.9	99	2 S26899	Ig heavy chain V r
28	452	73.6	135	2 S31604	Ig heavy chain V r
29	451	73.5	118	2 S20780	Ig heavy chain V r

30	451	73.5	129	2 S44114	Ig heavy chain V r
31	448	73.0	99	2 S12418	Ig heavy chain V r
32	447.5	72.9	139	2 S31696	Ig heavy chain V r
33	445.5	72.6	137	2 S31585	Ig heavy chain V r
34	445.5	72.6	140	2 A49045	Ig heavy chain V r
35	445	72.5	120	2 PT0370	Ig mu chain precu
36	444	72.3	126	2 S47010	Ig heavy chain V4.
37	443	72.1	99	2 S26800	Ig heavy chain V r
38	442	72.0	99	2 S12412	Ig heavy chain V r
39	442	72.0	105	2 S44125	Ig lambda chain V
40	442	72.0	118	2 S24443	Ig heavy chain V r
41	442	72.0	140	2 S78052	Ig heavy chain pre
42	441.5	71.9	98	2 S12421	Ig heavy chain V r
43	441.5	71.9	132	2 A38911	Ig heavy chain V r
44	441.5	71.9	140	2 A24770	hypothetical hybr
45	441	71.8	97	2 S26906	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S78051 Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C:Accession: S78051; S23716

R:Harindranath, N.
submitted to the EMBL Data Library, August 1990

A:Reference number: S78051

A:Accession: S78051

A:Molecule type: mRNA

A:Residues: 1-135 <HAR>

A:Cross-references: EMBL:X54437; NID:937814; PIDN:CAA38306.1; PID:9330117

R:Harindranath, N.; Goldfarb, I.; S. Iikematsu, H.; Burastero, S.E.; Wilder, R.L.; Nockins

Int. Immunol. 3, 865-875, 1991

A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and hu

patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404

A:Accession: S23716

A:Molecule type: mRNA

A:Residues: 13-111 <HAW>

A:Cross-references: EMBL:X54437

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:1-13/Domain: signal sequence (fragment) #status predicted <SIG>

F:14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>

F:27-111/Domain: immunoglobulin homology <IMW>

Query Match 81.7%; Score 501.5; DB 2; Length 135;
Best Local Similarity 82.2%; Pred. No. 2.4e-38;
Matches 97; Conservative 6; Mismatches 10; Indels 5; Gaps 2;

QY 2 EBSGGLVKSQSLTCTVSGGSIRSGYWSWIRPGKLEWIGYVSGNTYVPSL 61
DB 18 EBSGGLVKSQSLTCTVSGGSIRSGYWSWIRPGKLEWIGYVSGNTYVPSL 77
QY 62 KSRVTMSVDSKKNFSLRLSSVTAADTAAYVYCAR--SDGYTLDN---WGQGLTVTVSS 114
DB 78 KSRVTISVDSKKNFSLRLSSVTAADTAAYVYCARLGPDDYTLDMQDWDWGQGLTVTVSS 135

RESULT 2

S13519 Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S13519

R:Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.

Nucleic Acids Res. 19, 673, 1991

A:Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked

A:Reference number: S13519; MUID:91187691; PMID:2011536

A:Accession: S13519

A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-147 <MOR>
 A:Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:41-125/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 497.5; DB 2; Length 147;
 Best Local Similarity 82.8%; Pred. No. 66-38;
 Matches 96; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

QY 2 ESGPGLVKSQTLSTCTVSGGSIIRSGGYWMSIRPPGKGLMIGIYHSGNTYNNPSL 61
 DB 32 ESGPGLVKSQTLSTCTVSGGSIIRSGGYWMSIRPPGKGLMIGIYHSGNTYNNPSL 91

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDG-----DGYTLDMNGQGLVTYSS 114
 DB 92 KSRVTISVDTSKNQFSLKLSSTVADTAVYYCARPILMFGELFDYGGQGLVTYSS 147

RESULT 3

Ig variable region (VDJ) (clone T23-9) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
 C:Accession: J37782; S25476
 R:Demaison, C.; Chateigner, P.; Theze, J.; Zouali, M.
 Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
 A>Title: Somatic diversification in the heavy chain variable region genes expressed by B
 A:Reference number: A36876; MID:94119917; PMID:8290556
 A:Accession: J37782
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-140 <RES>
 A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:46-128/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 492.5; DB 2; Length 140;
 Best Local Similarity 82.2%; Pred. No. 1.6e-37;
 Matches 97; Conservative 6; Mismatches 8; Indels 7; Gaps 2;

QY 2 ESGPGLVKSQTLSTCTVSGGSIIRSGGYWMSIRPPGKGLMIGIYHSGNTYNNPSL 61
 DB 25 ESGPGLVKSQTLSTCTVSGGSIIRSGGYWMSIRPPGKGLMIGIYHSGNTYNNPSL 82

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDG-----GYTLDMNGQGLVTYSS 114
 DB 83 KSRVTISVDTSKNQFSLKLSSTVADTAVYYCARHNSSSWYGRYFDYWGQGLVTYSS 140

RESULT 4

Ig heavy chain V region - human
 C:Species: Homo sapiens (man)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
 C:Accession: S30534
 R:Marlette, X.
 submitted to the EMBL Data Library, October 1992
 A:Reference number: S30520
 A:Accession: S30534
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-130 <MAR>
 A:Cross-references: EMBL:Z18320
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 79.8%; Score 490; DB 2; Length 130;
 Best Local Similarity 78.4%; Pred. No. 2.5e-37;
 Matches 98; Conservative 4; Mismatches 11; Indels 12; Gaps 2;

QY 2 ESGPGLVKSQTLSTCTVSGGSIIRSGGYWMSIRPPGKGLMIGIYHSGNTYNNPSL 61
 DB 6 ESGPGLVKSQTLSTCTVSGGSIIRSGGYWMSIRPPGKGLMIGIYHSGNTYNNPSL 65
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDG-----YT-----LDNWQGLT 109
 DB 66 KSRVTISVDTSKNQFSLKLSSTVADTAVYYCARDKGFGFGYGRNRAAFDIWGQGLT 125
 QY 110 VTSS 114
 DB 126 VTSS 130

Query Match 79.6%; Score 488.5; DB 2; Length 116;
 Best Local Similarity 81.2%; Pred. No. 3e-37;
 Matches 95; Conservative 7; Mismatches 6; Indels 9; Gaps 2;

QY 6 GLVKSQTLSTCTVSGGSIIRSGGYWMSIRPPGKGLMIGIYHSGNTYNNPSL 65
 DB 1 GLVKSQTLSTCTVSGGSIIRSGGYWMSIRPPGKGLMIGIYHSGNTYNNPSL 60

QY 66 TMSVDTSKNHFSLRLSSVTADTAVYYCARSDG-----LDNWQGLT 114
 DB 61 TISVDTSKNQFSLKLSSTVADTAVYYCARG-GYGYGYYYYVDMWGQGLT 116

RESULT 6

Ig heavy chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S31690
 R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Pougereau, M.; Tonnelle, C.
 submitted to the EMBL Data Library, June 1992
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A:Reference number: S31585
 A:Accession: S31690
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-130 <CU1>
 A:Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:20-102/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 487.5; DB 2; Length 130;
 Best Local Similarity 78.7%; Pred. No. 4.2e-37;
 Matches 96; Conservative 5; Mismatches 10; Indels 11; Gaps 2;

QY 2 ESGPGLVKSQTLSTCTVSGGSIIRSGGYWMSIRPPGKGLMIGIYHSGNTYNNPSL 61
 DB 11 ESGPGLVKSQTLSTCTVSGGSIIRSGGYWMSIRPPGKGLMIGIYHSGNTYNNPSL 68

Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996

C/Accession: S09711
 R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coatswell, J.
 Biochem. J. 268, 135-140, 1990
 A>Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of
 A/Reference number: S09710; M0ID:90262535; PMID:2111699
 A/Accession: S09711
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1146 <HUG>
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C/Keywords: heterotetramer; Immunoglobulin
 F/34-118/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 473.5; DB 2; Length 146;
 Best Local Similarity 73.8%; Pred. No. 8.7e-36;
 Matches 90; Conservative 10; Mismatches 13; Indels 9; Gaps 1;
 QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPKGLKLEWIGYIHSGNTYYPNL 61
 DB 25 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPKGLKLEWIGYIHSGNTYYPNL 84
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYCAR-----SDGYTLDNWGQGLTVTV 112
 DB 85 KSRVTMSVDTSKNHFSLRLSSVTADTAVYCARVIVSRISQSYMDVMGKGLTVTV 144
 QY 113 SS 114
 DB 145 SS 146

RESULT 12

S19668
 Ig heavy chain V region (VH4DH6) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000
 C/Accession: S19668; S24445
 R:Marker, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
 A>Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
 A/Reference number: S19663; M0ID:92085276; PMID:1748994
 A/Accession: S19668
 A/Molecule type: mRNA
 A/Residues: 1-127 <MAR>
 A/Cross-references: EMBL:X61648
 R:Jones, P.T.
 Submitted to the EMBL Data Library, October 1991
 A/Reference number: S24442
 A/Accession: S24445
 A/Molecule type: mRNA
 A/Residues: 1-118 'B', 120-121 'T', 123-126 'F' <JON>
 A/Cross-references: EMBL:X61648; NID:937722; PIDN:CAA3829.1; PID:91335380
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 127;
 Best Local Similarity 74.6%; Pred. No. 9.2e-36;
 Matches 91; Conservative 9; Mismatches 13; Indels 9; Gaps 1;
 QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPKGLKLEWIGYIHSGNTYYPNL 61
 DB 6 QSGSGLVKPSQTLSTCTVSGSIRSGGYWMIROPKGLKLEWIGYIHSGNTYYPNL 65
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYCARSDG-----YTLDNWGQGLTVTV 112
 DB 66 KSRVTMSVDTSKNHFSLRLSSVTADTAVYCARSDG-----YTLDNWGQGLTVTV 125
 QY 113 SS 114
 DB 126 SS 127

RESULT 13

S31514
 Ig heavy chain - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C/Accession: S31514
 R:Chastagner, P.; Demaison, C.; These, J.; Zouali, M.
 submitted to the EMBL Data Library, December 1992
 A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
 A/Reference number: S31509
 A/Accession: S31514
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-128 <CHA>
 A/Cross-references: EMBL:X69862; NID:933086; PIDN:CAA49496.1; PID:933087
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C/Keywords: heterotetramer; Immunoglobulin
 F/22-106/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 128;
 Best Local Similarity 78.4%; Pred. No. 9.3e-36;
 Matches 91; Conservative 8; Mismatches 14; Indels 3; Gaps 1;
 QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPKGLKLEWIGYIHSGNTYYPNL 61
 DB 13 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPKGLKLEWIGYIHSGNTYYPNL 72
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYCAR---SDGYTLDNWGQGLTVTV 114
 DB 73 KSRVTMSVDTSKNHFSLRLSSVTADTAVYCARVIVSRISQSYMDVMGKGLTVTV 128

RESULT 14

S31676
 Ig heavy chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C/Accession: S31676
 R:Guttmann, A.M.; Gauchier, L.; Boublil, L.; Fougereau, M.; Tonnel, C.
 submitted to the EMBL Data Library, June 1992
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A/Reference number: S31585
 A/Accession: S31676
 A/Molecule type: mRNA
 A/Status: preliminary
 A/Residues: 1-137 <CUI>
 A/Cross-references: EMBL:Z14182; NID:931031; PIDN:CAA76551.1; PID:931032
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/34-116/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 472; DB 2; Length 137;
 Best Local Similarity 82.6%; Pred. No. 1.1e-35;
 Matches 95; Conservative 4; Mismatches 12; Indels 4; Gaps 2;
 QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPKGLKLEWIGYIHSGNTYYPNL 61
 DB 25 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPKGLKLEWIGYIHSGNTYYPNL 82
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYCARSDG-----YTLDNWGQGLTVTV 114
 DB 83 KSRVTMSVDTSKNHFSLRLSSVTADTAVYCARSDG-----YTLDNWGQGLTVTV 137

RESULT 15

S26803
 Ig heavy chain V region - human
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C/Accession: S26803
 R:Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
 Eur. J. Immunol. 22, 1075-1082, 1992
 A>Title: Polymorphism of human immunoglobulin V(H) 4 germ-line genes.
 A/Reference number: S26800; M0ID:92201299; PMID:1348029

A: Accession: S26803
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-99 <MEN>
A: Cross-references: EMBL: Z14238; NID: g377710; PIDD: CA78607.1; PID: g1335374
C: Superfamily: immunoglobulin V region; immunoglobulin homology
C: Keywords: heterotrimer; immunoglobulin
F: 15-99/Domain: immunoglobulin homology <IMM>

	Query Match	76.4%	Score 469;	DB 2;	Length 99;
	Best Local Similarity	92.6%;	Pred. No. 1.5e-35;		
	Matches 87;	Conservative 4;	Mismatches 3;	Indels 0;	Gaps 0;
QY	2	ESGPELVKPSQTLSLTCTVSGSINSGGYMWNIROPCKGLKLEWIGLIYHSNTYYNSL	61		
Db	6	ESGPELVKPSQTLSLTCTVSGSISGGYMWNIROPCKGLKLEWIGLIYSGSTYYNSL	65		
QY	62	KSRVTMSVDTSKNHFSLRLSSVTADPTAVYYCAR	95		
Db	66	KSRVTISVDTSKNQPSLKLISSVTADPTAVYYCAR	99		

Search completed: February 10, 2004, 18:41:09
Job time : 12.7455 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 17:48:48 ; Search time 6.39091 Seconds
(without alignments)
838.855 Million cell updates/sec

Title: US-10-027-725A-9

Sequence: 1 LESGGLVPSQTLSTCTV.....RSDGTYLDNMGGTLVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	439.5	71.6	129	1	HV2F_HUMAN
2	420	68.4	146	1	HV2I_HUMAN
3	393.5	64.1	117	1	HV2G_HUMAN
4	372.5	60.7	137	1	HV46_MOUSE
5	357.5	58.2	113	1	HV47_MOUSE
6	349.5	56.9	144	1	HV43_MOUSE
7	348.5	56.8	116	1	HV61_MOUSE
8	347	56.5	117	1	HV62_MOUSE
9	342.5	55.8	116	1	HV60_MOUSE
10	330	53.7	135	1	HV02_XENLA
11	313	51.0	120	1	HV2B_HUMAN
12	302.5	49.3	119	1	HV2C_HUMAN
13	293.5	47.8	136	1	HV01_XENLA
14	291	47.4	122	1	HV3A_HUMAN
15	289.5	47.1	125	1	HV2D_HUMAN
16	289	47.1	114	1	HV3B_HUMAN
17	288	46.9	115	1	HV44_MOUSE
18	288	46.9	147	1	HV2H_HUMAN
19	287.5	46.8	121	1	HV2E_HUMAN
20	287	46.7	119	1	HV40_MOUSE
21	286.5	46.7	117	1	HV2B_RABIT
22	282	45.9	122	1	HV3G_HUMAN
23	280	45.6	126	1	HV2A_HUMAN
24	278	45.3	116	1	HV05_CARAU
25	277.5	45.2	121	1	HV3J_HUMAN
26	277	45.1	119	1	HV3J_HUMAN
27	276	45.0	116	1	HV45_MOUSE
28	276	45.0	116	1	HV45_MOUSE
29	275	44.8	136	1	HV2C_RABIT
30	274	44.6	114	1	HV38_MOUSE
31	272.5	44.4	117	1	HV2A_RABIT
32	272.5	44.4	117	1	HV41_MOUSE
33	272	44.3	122	1	HV42_MOUSE

34	271.5	44.2	142	1	HV01_RAT	P01805 ratus norv
35	268	43.6	139	1	HV07_MOUSE	P01751 mus musculu
36	263.5	42.9	115	1	HV3D_HUMAN	P01765 mus sapien
37	263	42.8	118	1	HV51_MOUSE	P06330 mus musculu
38	263	42.8	122	1	HV20_MOUSE	P01789 mus musculu
39	262.5	42.8	117	1	HV12_MOUSE	P01756 mus musculu
40	262	42.7	120	1	HV50_MOUSE	P06329 mus musculu
41	262	42.7	126	1	HV3K_HUMAN	P01772 homo sapien
42	262	42.7	136	1	HV16_MOUSE	P01783 mus musculu
43	261.5	42.6	115	1	HV3F_HUMAN	P01767 homo sapien
44	261.5	42.6	117	1	HV13_MOUSE	P01757 mus musculu
45	258.5	42.1	117	1	HV17_MOUSE	P01786 mus musculu

ALIGNMENTS

RESULT 1	ID	Query Match	Length	ID	Description
1	HV2F_HUMAN	71.6%	129	1	HV2F_HUMAN
AC	P01824	68.4%	146	1	HV2I_HUMAN
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Ig heavy chain V-II region MAH.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE.				
RA	MEDLINE=8222235; PubMed=680618;				
RA	Takanaishi N., Terauchi D., Debitte B., Lin L.-C., Putnam F.W.;				
RT	"Complete amino acid sequence of the delta heavy chain of human				
RT	immunoglobulin D.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).				
CC	-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA				
CC	PROTEIN.				
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.				
DR	PIR; A02099; D2HUMA.				
DR	HSSP; P01825; 7FAB.				
DR	GlycoSuiteDB; P01824; -.				
DR	GO; GO:0005576; C:extracellular; NAS.				
DR	GO; GO:0003823; F:antigen binding activity; NAS.				
DR	GO; GO:0006955; P:immune response; NAS.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003006; Ig-MHC.				
DR	InterPro; IPR003596; Ig-V.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; IGV_1.				
DR	PROSITE; PS50835; IG-LIKE; 1.				
KW	Immunoglobulin V region.				
FT	DOMAIN 1 113 IG-LIKE.				
FT	NON TER 129 129				
SQ	SEQUENCE 129 AA; 14117 MW; DSD53D47ABE51319 CRC64;				
Query Match	71.6%; Score 439.5; DB 1; Length 129;				
Best Local Similarity	66.7%; Pred. No. 4.2e-39;				
Matches	84; Conservative 12; Mismatches 15; Indels 15; Gaps 2;				
QY	2 ESSGGLVPSQTLSTCTVSGGSTRSGGYSMWRPQKGLWNGIYHSGNRYNPSL 61				
DB	6 ESSGGLVPSQTLSTCTVSGGSTRSGGYSMWRPQKGLWNGIYHSGNRYNPSL 65				
QY	62 KSRVTMSVDTSKNPSLRSLSSVTAAADTAIVYCAR-----SDGTYLDNMGGGT 108				
DB	66 KGRVTISVDTSRNPSLRSLSSVTAAADTAIVYCAR-----SDGTYLDNMGGGT 123				
QY	109 LVTVSS 114				
DB	124 TVHVS 129				

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RESULT 2
HV21 HUMAN
ID HV21 HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85205332; PubMed=3922855;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RL Gene 33:181-189 (1985).
DR PIR: A02101; GIHDR2.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.
FT DOMAIN 20 117 V SEGMENT.
FT DOMAIN 118 127 D SEGMENT.
FT DOMAIN 128 146 J SEGMENT.
FT DISULFID 42 115 BY SIMILARITY.
FT NON TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match 68.4%; Score 420; DB 1; Length 146;
Best Local Similarity 71.1%; Pred. No. 5.3e-37;
Matches 86; Conservative 7; Mismatches 16; Indels 12; Gaps 3;

QY 4 GPGLVKPSQTLSTCTVSGSGSIRSGGYMSWIRPQPKGLEWIGYHSGNTYNSLKS 63
DB 28 GAGLVKPSQTLSTCTCAVFGGSF--SGYMSWIRPQPKGLEWIGYHSGNTYNSLKS 85
QY 64 RVTMSVDTSKNHFSLRLSVTAADTAVYYCARS---DG-----YTLDMWGQGLVTVSS 113
DB 86 RVTISLDTSKNLFSLKLSSTVTAADTAVYYCARGLLGGKMDVDVYYGMDVWGQGLTVTVSS 145
QY 114 S 114
DB 146 S 146

RESULT 3
HV2G HUMAN
ID HV2G HUMAN STANDARD; PRT; 117 AA.
AC P01825;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region NEMM.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77242302; PubMed=407927;
RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;

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RT "Amino acid sequence of the VH region of a human myeloma
RL immunoglobulin (IG New).";
RL Biochemistry 16:3412-3420 (1977).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
RX MEDLINE=78066916; PubMed=618887;
RA Saul F.A., Amel L.M., Poljak R.J.;
RT "Preliminary refinement and structural analysis of the Fab fragment
RT from human immunoglobulin new at 2.0-A resolution.";
RL J. Biol. Chem. 253:585-597 (1978).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGGI MYELOMA
CC PROTEIN.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A90404; GIHUM.
DR PDB; 7FAB; 31-JAN-94.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; 3d-structure; Pyrrolidone carboxylic acid.
FT DOMAIN 1 111
FT MOD RES 1 111
FT STRAND 3 7
FT TURN 11 12
FT TURN 14 15
FT STRAND 18 25
FT TURN 30 31
FT STRAND 33 39
FT TURN 41 42
FT STRAND 46 51
FT TURN 53 54
FT STRAND 57 59
FT HELIX 61 63
FT TURN 64 66
FT STRAND 67 72
FT TURN 73 76
FT STRAND 77 82
FT HELIX 87 89
FT STRAND 91 98
FT STRAND 104 107
FT STRAND 111 115
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;

Query Match 64.1%; Score 393.5; DB 1; Length 117;
Best Local Similarity 67.5%; Pred. No. 2.4e-34;
Matches 77; Conservative 16; Mismatches 16; Indels 3; Gaps 2;

QY 2 ESGPGLVKSQTLSTCTVSGSGSIRSGGYMSWIRPQPKGLEWIGYHSGNTYNSL 61
DB 6 QSGPGLVKSQTLSTCTVSGSGTFSND--YYTWVQRPQPKGLEWIGYHSGTSDTTP 63
QY 62 KSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARS--DG-----YTLDMWGQGLVTVSS 114
DB 64 RSRVTMLVDTSKNHFSLRLSVTAADTAVYYCARNLIGCIDVWGQGLTVTVSS 117

RESULT 4
HV46 MOUSE
ID HV46 MOUSE STANDARD; PRT; 137 AA.
AC P01822;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain V region MOPC 315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=89238351; PubMed=2497341;
 RA Ralfert A., Horne C., Dorrington K.J., Klein M.;
 "Cloning, sequencing and expression of the rearranged MOPC 315 VH
 gene segment";
 RL Mol. Immunol. 26:431-434 (1989).
 [2]
 SEQUENCE OF 1-31.
 RX MEDLINE=78094475; PubMed=414225;
 RA Jilka R.L., Pestka S.;
 "Amino acid sequence of the precursor region of MOPC-315 mouse
 immunoglobulin heavy chain";
 RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).
 [3]
 SEQUENCE OF 1-21.
 RX MEDLINE=79148758; PubMed=428562;
 RA Schechter I., Wolf O., Zemel R., Burstein Y.;
 "Structure and function of immunoglobulin genes and precursors";
 RL Fed. Proc. 38:1839-1845 (1979).
 [4]
 SEQUENCE OF 19-136.
 RX MEDLINE=74170779; PubMed=4524622;
 RA Francis S.H., Leslie R.G.O., Hood L., Eisen H.N.;
 "Amino acid sequence of the variable region of the heavy (alpha)
 chain of a mouse myeloma protein with anti-hapten activity";
 RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127 (1974).
 [5]
 REVISION TO 53.
 RX MEDLINE=77244979; PubMed=268248;
 RA Hood L., Margolies M.N., Givol D., Zakut R.;
 Unpublished results, cited by:
 RL Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
 Cold Spring Harb. Symp. Quant. Biol. 41:627-637 (1976).
 CC -!- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
 PROTEIN THAT HAS ANTI-DINITROBENZYL ACTIVITY.

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 CC EMBL; M27638; AAA61337.1; -;
 DR EMBL; X07880; CA30727.1; -;
 DR PIR; P0102; AVMS35.
 DR HSSP; P01825; 7EAB.
 DR InterPro; IPR007110; 1g-1like.
 DR InterPro; IPR003006; 1g_MHC.
 DR InterPro; IPR003596; 1g_v.
 DR Pfam; PF00047; 1g_1.
 DR SMART; SM00406; 1g_v.1.
 DR PROSITE; PS50835; 1g_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 18
 FT CHAIN 1 137 IG HEAVY CHAIN V REGION MOPC 315.
 FT DOMAIN 19 48 FRAMEWORK-1.
 FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 85 116 FRAMEWORK-3.
 FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 127 137 FRAMEWORK-4.
 FT DISULFID 40 114 BY SIMILARITY.
 FT CONFLICT 15 15 G-> GG (IN REF. 1; CAA30727).
 FT CONFLICT 15 15 G-> H (IN REF. 2).
 FT CONFLICT 77 78 GY-> YG (IN REF. 4).
 FT CONFLICT 102 102 N-> D (IN REF. 4).
 FT CONFLICT 123 123 MISSING (IN REF. 4).
 FT NON_TER 137 137

SEQ SEQUENCE 137 AA; 1539 MW; FB3828304C2B81DC CRC64;
 Query Match 60.7%; Score 372.5; DB 1; Length 137;
 Best Local Similarity 62.6%; Pred. No. 4.6e-32;
 Matches 71; Conservative 16; Mismatches 22; Indels 3; Gaps 2;
 QY 2 ESGGGLVPSQTLTLCTVSGSGSIRSGGYWMTROPFGKLEWIGYIYHSGNTYNSPL 61
 DB 6 ESGGGLVPSQTLTLCTVSGSGSIRSGGYWMTROPFGKLEWIGYIYHSGNTYNSPL 63
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYCARSDG--YTLDNWGCGTLVTYSS 114
 DB 24 ESGGGLVPSQSLTSLTSGSVGYSTLS--GYFMNWRQFGPKKLEWIGIKYDGSNGYNPSL 82
 QY 83 KNRVSIKTRDTSNQFPLKNSVTTEDTATYTCAGDNHLYFDYWGCGTLVTYSS 137
 RESULT 5
 ID HV47 MOUSE STANDARD; PRT; 113 AA.
 AC P01823;
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 36-60.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=84024551; PubMed=6414509;
 RA Juzczak E.C., Margolies M.N.;
 "Amino acid sequence of the heavy chain variable region from the A/J
 mouse anti-arsenate monoclonal antibody 36-60 bearing a minor
 idiotype";
 RL Biochemistry 22:4291-4296 (1983).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTARSONATE
 MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND
 IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTARSONATE RESPONSE OF
 STRAIN A/J MICE.
 CC CC
 CC PIR; A02098; G2MS60.
 DR PDB; 1J10; 18-FEB-03.
 DR PDB; 1J1P; 18-FEB-03.
 DR PDB; 1J1X; 18-FEB-03.
 DR InterPro; IPR007110; 1g-1like.
 DR InterPro; IPR003006; 1g_MHC.
 DR InterPro; IPR003596; 1g_v.
 DR Pfam; PF00047; 1g_1.
 DR SMART; SM00406; 1g_v.1.
 DR PROSITE; PS50835; 1g_LIKE; 1.
 DR Immunoglobulin V region; 3D-structure.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12734 MW; 38DC0BE3F5075B7 CRC64;
 Query Match 58.2%; Score 357.5; DB 1; Length 113;
 Best Local Similarity 62.8%; Pred. No. 1.4e-30;
 Matches 71; Conservative 16; Mismatches 21; Indels 5; Gaps 2;
 QY 2 ESGGGLVPSQTLTLCTVSGSGSIRSGGYWMTROPFGKLEWIGYIYHSGNTYNSPL 61
 DB 6 ESGGGLVPSQTLTLCTVSGSGSIRSGGYWMTROPFGKLEWIGYIYHSGNTYNSPL 63
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYCARSDG--YTLDNWGCGTLVTYSS 114
 DB 64 KSRVSIKTRDTSNQFPLKNSVTTEDTATYTCAGDNHLYFDYWGCGTLVTYSS 113
 RESULT 6
 ID HV43 MOUSE STANDARD; PRT; 144 AA.
 AC P01819;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 141 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes."
RL Nature 286:676-683(1980).
CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL; V00768; CAA24149.1; -.
DR PIR; A02094; G2MS14.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR KX Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19
FT DOMAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.
FT NON_TER 20 130 IG-LIKE.
FT FT 144
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 56.9%; Score 349.5; DB 1; Length 144;
Best Local Similarity 59.0%; Pred. No. 1.2e-29;
Matches 72; Conservative 18; Mismatches 21; Indels 11; Gaps 3

OY 2 ESGPGLVAPSOQLSLTCTVSGSGSIRSGYVMSIRPKSGKGLWIGYIHSGNTYYNPSL 61
DB 25 ESGPGLVAPSOQLSLTCTVSGSFL--GYGVNVAQPPKSGLEWIGTIMGNSTDYNSLT 82
OY 62 KSRVTMSVDTSHNHPSLRISVTAADTAVTYCA-----RSDGY-TLDNGGGLTVTV 112
DB 83 KSRLLTITTDNSKRSQVFLKMNLSLOTDTIARYVCASVSIYYGSRSDKYFTLDYGCGTSVTV 142
OY 113 SS 114
DB 143 SS 144

RESULT 7
HVL_MOUSE STANDARD; PRT; 116 AA.
ID _HVL_MOUSE
AC P18532;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 1B43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/CJ;

```

RA	MEDLINE=69279149; PubMed=2499654;
RA	Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT	"Early onset of somatic mutation in immunoglobulin VH genes during
RT	the primary immune response."
RL	J. Exp. Med. 169:2007-2019(1989).
CC	-1. MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
DR	PIR; J05058; HVMS1B.
DR	PDB; 1KCV; 11-MAY-02.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_V.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SMO0406; IgV; 1.
DR	PROSITE; PSS0835; IG LIKE; 1.
DR	Immunoglobulin V region; Signal; 3D-structure.
FT	CHAIN 1
FT	SIGNAL 18
FT	CHAIN 19 116 IG HEAVY CHAIN V REGION 1B43.
FT	DOMAIN 19 48 FRAMEWORK-1.
FT	DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 54 67 FRAMEWORK-2.
FT	DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 85 116 FRAMEWORK-3.
FT	DISULFID 40 114 BY SIMILARITY.
FT	NON TER 116 116
SO	SEQUENCE 116 AA; 13158 MW; 1CB547255681FF74 CRC64;
Query Match	56.8%; Score 348.5; DB 1; Length 116;
Best Local Similarity	71.3%; Pred. No. 1.2e-29;
Matches 67; Conservative 11; Mismatches 15; Indels 1; Gaps 1;	
Oy	2 ESEGGVLPKPGTSLTCTVSGGSRSGGYVSWIRPGPKGLENGYTHSGNRYNPSL 61
Db	24 ESGGDLVKPSQSSLTCTVGYSTTS-GYSWHWIRPGPKLENGYTHSGNYSNPSL 82
Oy	62 KSRVTMSVDTSKNHFSLRLSSVTADPAVYYCAR 95
Db	83 KSRISITRDTSKNOFFQLNSVTTEDTATYYCAR 116
RESULT 8	
HV62_MOUSE	STANDARD; PRT; 117 AA.
ID	
AC	P18533;
DT	01-NOV-1990 (Rel. 16, Created)
DT	01-NOV-1990 (Rel. 16, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Ig heavy chain V region 733 precursor.
OS	Mus musculus (Mouse).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BALB/3J;
RX	MEDLINE=89279149; PubMed=2499654;
RA	Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT	"Early onset of somatic mutation in immunoglobulin VH genes during
RT	the primary immune response."
RL	J. Exp. Med. 169:2007-2019(1989).
CC	-1. SIMILARITY: Contains 1 immunoglobulin-like domain.
DR	PIR; J0510; HVMS73.
DR	HSSP; P01825; 7EAB.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_V.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SMO0406; IgV; 1.
DR	PROSITE; PSS0835; IG LIKE; 1.
KW	Immunoglobulin V region; Signal.
FT	SIGNAL 18
FT	CHAIN 19 117 IG HEAVY CHAIN V REGION 733.
FT	DOMAIN 19 >117 IG-LIKE.


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FT DISULFID 40 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13223 MW; 1595517821F976BE CRC64;

Query Match
Best Local Similarity 56.5%; Score 347; DB 1; Length 117;
Matches 65; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

OY 2 ESGPGLVPSQTLSTCTVSGSGSIRSGGYWMSWIRPQPKGLEWIGYHSGNTYYNSL 61
DB 24 ESGPGLVPSQSLSITCSVTGYSLTS-gywmwimiofpgnklemwgyisysdgsnnypsl 83

OY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYCAR 95
DB 84 KSRITITDTSKNOFPLEMNSLTAEITATYCAR 117

RESULT 9
HV60_MOUSE STANDARD; PRT; 116 AA.
ID HV60_MOUSE
AC P18531.
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region M315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/CI;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
DR PIR: J05059; HVM31.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT CHAIN 1 18
FT SIGNAL 1 18
FT DOMAIN 19 116 IG HEAVY CHAIN V REGION M315.
FT DOMAIN 49 53 FRAMEWORK-1.
FT DOMAIN 54 67 FRAMEWORK-2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON TER 116 116
SQ SEQUENCE 116 AA; 13095 MW; 4562E03E53DC9E10 CRC64;

Query Match
Best Local Similarity 55.8%; Score 342.5; DB 1; Length 116;
Matches 64; Conservative 14; Mismatches 15; Indels 1; Gaps 1;

OY 2 ESGPGLVPSQTLSTCTVSGSGSIRSGGYWMSWIRPQPKGLEWIGYHSGNTYYNSL 61
DB 24 ESGPGLVPSQSLSITCSVTGYSLTS-gywmwimiofpgnklemwgyisysdgsnnypsl 82

OY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYCAR 95
DB 83 KSRITITDTSKNOFPLEMNSLTAEITATYCAR 116

RESULT 10
HV02_XENLA STANDARD; PRT; 135 AA.
ID HV02_XENLA

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AC P20957;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region XIG14 precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoryk C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis Igm deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains."
RT Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC -I SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J03632; AAA49791.1; -.
CC PIR: B31933; B31933.
CC HSSP: P01810; 2FBJ.
CC InterPro: IPR007110; IG-1like.
CC InterPro: IPR003006; IG_MHC.
CC InterPro: IPR003596; IG_v.
CC Pfam: PF00047; Ig_1.
CC SMART: SM00406; IgV_1.
CC PROSITE: PS50835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
FT CHAIN 1 1
FT NON TER 1 1
FT SIGNAL 1 18
FT CHAIN 19 135 IG HEAVY CHAIN V REGION XIG14.
FT DOMAIN 20 128 IG-LIKE.
FT NON TER 135 135
SQ SEQUENCE 135 AA; 15080 MW; BEC467105C00732E CRC64;

Query Match
Best Local Similarity 53.7%; Score 330; DB 1; Length 135;
Matches 65; Conservative 16; Mismatches 30; Indels 4; Gaps 2;

OY 2 ESGPGLVPSQTLSTCTVSGSGSIRSGGYWMSWIRPQPKGLEWIGYHSGNTYYNSL 61
DB 23 ESGPGLVPSQSLSITCSVTGYSLTS-yhmwmwimiofpgnklemwgyisysdgsnnypsl 80

OY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYCAR--SDGYTLDMNGGTLVTVSS 114
DB 81 KSRITITDTSKNOFPLEMNSLTAEITATYCAR--GYNFYDYGQSTVTVTS 135

RESULT 11
HV2B_HUMAN STANDARD; PRT; 120 AA.
ID HV2B_HUMAN
AC P01815;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region COR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;

```

RA Press E.M., Hogg N.M.;
RT "the amino acid sequences of the Fd fragments of two human gamma-1
RT heavy chains."
RL Biochem. J. 117:641-660(1970).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02089; GIHUCO.
DR HSSP: P01825; 7FAB.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Glycoprotein; Pyrrolidone carboxylic acid.
FT MOD_RES 1 110
FT DISULFID 22 94
FT CARBOHYD 62 62
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13226 MW; 158A8B29AE7EEB98 CRC64;
Query Match 51.0%; Score 313; DB 1; Length 120;
Best Local Similarity 56.3%; Pred. No. 6; 6e-26;
Matches 67; Conservative 13; Mismatches 29; Indels 10; Gaps 3;
QY 2 ESGPGVLRKPSQTLSTCTVSGSIRSGYWMIRPPCKGLEWIGYIHSGNTYNNPSL 61
DB 6 ESGPVLVRPTQTLTCTFSGFSLSGTMCVMGIRPPCKGLEWLRIMDDDKXTNTSL 65
QY 62 KSRVTSVDTSKNHSRLRSLSTVADTAVYVCARSDG--YTLDMGQGLTVTVSS 114
DB 66 ETRLTISKDTSRKNQVVLTMDPV---DTATYCARITVTPAPAGY-MDVWGRTPTVTVSS 120
RESULT 12
ID HV2C_HUMAN STANDARD; PRT; 119 AA.
AC P01816;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-II region DAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70258837; PubMed=5449120;
RA Press E.M., Hogg N.M.;
RT "the amino acid sequences of the Fd fragments of two human gamma-1
RT heavy chains."
RL Biochem. J. 117:641-660(1970).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGG1 ISOLATED FROM THE
CC SERUM OF A PATIENT WITH HYPERGAMMAGLOBULINEMIA.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02091; GIHUCO.
DR HSSP: P01789; IMCP.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Pyrrolidone carboxylic acid.

FT DOMAIN 1 113 IG-LIKE.
FT MOD_RES 1 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13045 MW; 4E13E00214BAD789 CRC64;
Query Match 49.3%; Score 302.5; DB 1; Length 119;
Best Local Similarity 53.5%; Pred. No. 8; 1e-25;
Matches 61; Conservative 17; Mismatches 35; Indels 1; Gaps 1;
QY 2 ESGPVLVRPTQTLSTCTFSGFSLSGTMCVMGIRPPCKGLEWLRIMDDDKXTNTSL 61
DB 6 ESGPVLVRPTQTLTCTFSGFSLSGTMCVMGIRPPCKGLEWLRIMDDDKXTNTSL 65
QY 62 KSRVTSVDTSKNHSRLRSLSTVADTAVYVCARSDG--YTLDMGQGLTVTVSS 114
DB 66 ETRLVSKDTSRKNQVVLTMDPV---DTATYCARITVTPAPAGY-MDVWGRTPTVTVSS 119
RESULT 13
ID HV01_XENLA STANDARD; PRT; 136 AA.
AC P20956;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region XIg8 precursor (fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxId=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoyak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis Igm deduced
RT from cDNA sequence: implications for evolution of immunoglobulin
RT domains."
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M20484; AAA49774.1; ALU_TERM.
DR PIR: A31933; A31933.
DR HSSP: P01825; 7FAB.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL 1 18
FT CHAIN 19 136 IG HEAVY CHAIN V REGION XIg8.
FT DOMAIN 19 128 IG-LIKE.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15123 MW; 3141839881441963 CRC64;
Query Match 47.8%; Score 293.5; DB 1; Length 136;
Best Local Similarity 52.1%; Pred. No. 8; 3e-24;
Matches 61; Conservative 18; Mismatches 31; Indels 7; Gaps 3;
QY 2 ESGPGLVRKPSQTLSTCTVSGSIRSGYWMIRPPCKGLEWIGYIHSGNTYNNPSL 61
DB 23 ESGPGLVRKPSQTLSTCTVSGFSLSGTMCVMGIRPPCKGLEWLRIMDDDKXTNTSL 80

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYC---ARSDQYTLDMNGGTLVTVSS 114
 DB 81 KNRVTITKDNKGKQVYQLQMGNEVKDYAMYYCTSTLGTAGI-FEHMGQTMVTVTS 136

RESULT 14

HV3A_HUMAN STANDARD; PRT; 122 AA.

AC P01762;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V-II region TRO.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE (MYELOMA PROTEIN TRO).

RK MEDLINE=76023781; PubMed=809331;

RA Kratzin H., Altevogt P., Ruban E., Kortt A., Starosck K.,

RA Hilschmann N.;

RT "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.),

RT II. The amino acid sequence of the H-chain, alpha-type, subgroup III;

RT structure of the complete IgA-molecule." (1975).

RL Hoppe-Seyler S.Z. Physiol. Chem. 356:1337-1342(1975).

CC -I- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.

CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR: A02045; A1HUTR.

DR HSSP: P01772; 2P84.

DR GO: GO:0005576; C:extracellular; NAS.

DR GO: GO:0003823; F:antigen binding activity; NAS.

DR GO: GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; Ig_Like.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IGV; 1.

DR PROSITE: PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Pyrrolidone carboxylic acid.

FT DOMAIN 1 108 IG-LIKE.

FT MOD_RES 1 108 PYRROLIDONE CARBOXYLIC ACID.

FT NON_TER 122 122

SO SEQUENCE 122 AA; 13472 MW; 2E21A11DA04D80F9 CRC64;

Query Match 47.4%; Score 291; DB 1; Length 122;
 Best Local Similarity 47.5%; Pred. No. 1.3e-23;
 Matches 57; Conservative 22; Mismatches 33; Indels 8; Gaps 3;

QY 1 EESGGLVLPESQTLSLTCTVSGSIRSGGYWMTROPKGLKLEWIGYIHSGNT-YYNP 59
 DB 5 VQSGGGLVLPESQTLSLTCTVSGSIRSGGYWMTROPKGLKLEWIGYIHSGNT-YYNP 62
 QY 60 SLKSVYMSVDTSKNHFSLRLSSVTADTAAYVYCARSDC-----YTLDMNGGTLVTVSS 114
 DB 63 SVKGRFTISRDAQKSLYLZMBSLRTBTAAYVYCAATBFBWSTSLBYMGZGLVTVSS 122

RESULT 15

HV2D_HUMAN

AC P01817; STANDARD; PRT; 125 AA.

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V-II region MCB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=81118242; PubMed=6780622;
 RA Geber-Jenson B., Kazin A., Kehoe J.M., Scheffel C., Erickson B.W.,
 RA Lieberman G.W.;
 RT "Molecular basis for the temperature-dependent insolubility of
 RT cryoglobulins. X. The amino acid sequence of the heavy chain variable
 RT region of MCB.";
 RL J. Immunol. 126:1212-1216(1981).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS DERIVED FROM A MONOCLONAL IGM
 CC CRYOIMMUNOGLOBULIN.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02092; MHHUMC.
 DR HSSP: P01825; 7PAB.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 113 IG-LIKE.
 FT MOD_RES 1 113 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 125 125
 SO SEQUENCE 125 AA; 13783 MW; 7A1ADP4C40F47BB5 CRC64;

Query Match 47.1%; Score 289.5; DB 1; Length 125;
 Best Local Similarity 47.5%; Pred. No. 2e-23;
 Matches 57; Conservative 20; Mismatches 36; Indels 7; Gaps 1;
 QY 2 EESGGLVLPESQTLSLTCTVSGSIRSGGYWMTROPKGLKLEWIGYIHSGNTYYNP 61
 DB 6 EESGGLVLPETTLTLCTFSGSFLSTSGVGWGTROPKGLKLEWLAFLNDDNNRYSFSL 65
 QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAAYVYCARSDCGT-----LDNMGGTLVTVSS 114
 DB 66 RSRITGFTISRDAQKSLYLZMBSLRTBTAAYVYCAATBFBWSTSLBYMGZGLVTVSS 125

Search completed: February 10, 2004, 18:36:30
 Job time : 6.39091 secs

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DB 6 ESGPGLVKSPTSLCTCTVSGGSGS--YVSMWIRQPGKGLMWIGYIYSGSTNTPSL 63
QY 62 KSRVTMSVDTSKNHSRLSSVTAAADTAVYYCARSG---YTDNMGCGTLVTYSS 114
DB 64 KSRVTISVDTSKNQFSLKLTSLTAADTAVYFCARLSNMGYPYDYGCGTLVTYSS 119

RESULT 2
ID 095973 PRELIMINARY; PRT; 150 AA.
AC 095973;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE V44 heavy chain variable region precursor (Fragment).
GN IGM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCHI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT "Clonal proliferation of IGM secreting B cell in the synovium of
RT Rheumatoid arthritis patient with arthritis."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103195; AAC79084.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 >150 V44 HEAVY CHAIN VARIABLE REGION.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AATC9 CRC64;

Query Match 76.2%; Score 468; DB 4; Length 150;
Best Local Similarity 78.8%; Pred. No. 3e-41;
Matches 89; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 2 ESGPGLVKSPTSLCTCTVSGGSGSIRSGGYWMSIRQPGKGLMWIGYIYSGSTNTPSL 61
DB 25 ESGPGLVKSPTSLCTCTVSGGSGSISSTNYWGWIRQPGKGLMWISGLHNSGSDYNNPSL 84

QY 62 KSRVTMSVDTSKNHSRLSSVTAAADTAVYYCARSDGYTLNMGCGTLVTYSS 114
DB 85 KSRVTISVDTSKNQFSLKLTSLTAADTAVYFCARLKGAFDFGHTMTYSS 137

RESULT 3
ID 096KX8 PRELIMINARY; PRT; 496 AA.
AC 096KX8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCHI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAH16369.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 74.9%; Score 460; DB 4; Length 496;
Best Local Similarity 75.0%; Pred. No. 9.2e-40;
Matches 90; Conservative 8; Mismatches 14; Indels 8; Gaps 2;

QY 2 ESGPGLVKSPTSLCTCTVSGGSGSIRSGGYWMSIRQPGKGLMWIGYIYSGSTNTPSL 61
DB 25 ESGPGLVKSPTSLCTCTVSGGSGSISSTNYWGWIRQPGKGLMWISGLHNSGSDYNNPSL 84

QY 62 KSRVTMSVDTSKNHSRLSSVTAAADTAVYYCARSDGYT-----LDNMGCGTLVTYSS 114
DB 85 KSRVTISVDTSKNQFSLKLTSLTAADTAVYFCAR-HGYSRSGRTGADYWGCGTLVTYSS 143

RESULT 4
ID 096EY0 PRELIMINARY; PRT; 613 AA.
AC 096EY0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCHI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011857; AAH11857.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 74.9%; Score 460; DB 4; Length 613;
Best Local Similarity 80.5%; Pred. No. 1.2e-39;
Matches 95; Conservative 4; Mismatches 11; Indels 8; Gaps 3;

QY 2 ESGPGLVKSPTSLCTCTVSGGSGSIRSGGYWMSIRQPGKGLMWIGYIYSGSTNTPSL 61
DB 25 ESGPGLVKSPTSLCTCTVSGGSGS--YVSMWIRQPGKGLMWIGYIYSGSTNTPSL 82

QY 62 KSRVTMSVDTSKNHSRLSSVTAAADTAVYYCARSDGYTLN-----WCGTLYTVSS 114
DB 83 KSRVTMSVDTSKNQFSLKLTSLTAADTAVYCA-SQPWELPTVGLFWGCGTLVTYSS 139

RESULT 5
ID 081ZD7 PRELIMINARY; PRT; 130 AA.
AC 081ZD7;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Anti-thyroglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

Q9BU10 PRELIMINARY; PRT; 597 AA

OY

4 GPGILVPSQTLSTLCITYSGGSIRSGGYWMSIIROPKGLLEWIGVIYHSGNTYYNPSLKS 63
| | : ||| : ||||| | ||| ||||||||| ||||| | ||| : | |||||

Db 27 GAGLAKPSETLSLTCGVGGSS--SGYVMWIRQPPGKLEWIGELINSHSGSTNYNPSLKS 84
QY 64 RVTMSVDTSKNHSLSLSTCTVSGGSSIRSGYVMWIRQPPGKLEWIGELINSHSGSTNYNPSL 114
DB 85 RVTISVDTSKKQLSLKLSVYNADTAIVYCARVITRASPGTDRYGMVDWVGCGTIVTVSS 144

RESULT 9
ID 09B08 PRELIMINARY; PRT; 597 AA.
AC 09B08; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle, and Lymph.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -
DR EMBL; BC001872; AAH01872.1; -
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 69.3%; Score 425.5; DB 4; Length 597;
Best Local Similarity 72.5%; Pred. No. 4; ee-36;
Matches 87; Conservative 6; Mismatches 16; Indels 11; Gaps 3;

QY 4 GPGLVKPSQTLSTCTVSGGSSIRSGYVMWIRQPPGKLEWIGELINSHSGSTNYNPSLKS 63
DB 27 GAGLAKPSETLSLTCGVGGSS--SGYVMWIRQPPGKLEWIGELINSHSGSTNYNPSLKS 84
QY 64 RVTMSVDTSKNHSLSLSTCTVSGGSSIRSGYVMWIRQPPGKLEWIGELINSHSGSTNYNPSL 114
DB 85 RVTISVDTSKKQLSLKLSVYNADTAIVYCARVITRASPGTDRYGMVDWVGCGTIVTVSS 144

RESULT 10
ID 08TC63 PRELIMINARY; PRT; 473 AA.
AC 08TC63; 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER BLUE; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 67.1%; Score 412; DB 4; Length 473;
Best Local Similarity 69.0%; Pred. No. 9; ee-35;
Matches 80; Conservative 11; Mismatches 19; Indels 6; Gaps 2;

QY 2 ESGPGLVPSQTLSTCTVSGGSSIRSGYVMWIRQPPGKLEWIGELINSHSGSTNYNPSL 61
DB 32 ESGPGLKRSVTLSTCTVSGGSSIRSGYVMWIRQPPGKLEWIGELINSHSGSTNYNPSL 91
QY 62 KSRVMSVDTSKNHSLSLSTCTVSGGSSIRSGYVMWIRQPPGKLEWIGELINSHSGSTNYNPSL 113
DB 92 RSRVMSADMSENSEFLKLSVYNADTAIVYCARVITRASPGTDRYGMVDWVGCGTIVTVSS 145

RESULT 11
ID 099M22 PRELIMINARY; PRT; 479 AA.
AC 099M22; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002091; AAH02091.1; -
DR HSSP; P01810; 2FBD.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;

Query Match 63.9%; Score 392.5; DB 11; Length 479;
Best Local Similarity 67.5%; Pred. No. 1e-32;
Matches 77; Conservative 16; Mismatches 18; Indels 3; Gaps 3;

QY 2 ESGPGLVPSQTLSTCTVSGGSSIRSGYVMWIRQPPGKLEWIGELINSHSGSTNYNPSL 61
DB 24 ESGPGLVPSQTLSTCTVSGGSSIRSGYVMWIRQPPGKLEWIGELINSHSGSTNYNPSL 82
QY 62 KSRVMSVDTSKNHSLSLSTCTVSGGSSIRSGYVMWIRQPPGKLEWIGELINSHSGSTNYNPSL 114
DB 83 KSRVMSVDTSKNHSLSLSTCTVSGGSSIRSGYVMWIRQPPGKLEWIGELINSHSGSTNYNPSL 135

RESULT 12
ID 09UL75 PRELIMINARY; PRT; 122 AA.
AC 09UL75; 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.


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OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035039; AAD56275.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig_1-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13719 MW; 56CB0612586A6529 CRC64;

Query Match
Best Local Similarity 59.3%; Score 364; DB 4; Length 122;
Matches 72; Conservative 13; Mismatches 28; Indels 4; Gaps 2;

QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWIRPPGKGLWIGYIHSNTY--YNP 59
DB 6 QSGPGLVPSQTLSTCTCAISGDSVSSNSAMWMIQSPSGRLWIGYIHSNTYNDYRV 65

QY 60 SLKSVTVSVDPSKHFSLRLSVTAADTAAYVYCARSDGY--TLDMNGGTLVTVSS 114
DB 66 SVKSRITINPDSIKQFSLQNLNSVTPEDTAAYVYCARDELGLQGFYWGQGLTVTVSS 122

RESULT 13
Q9UL96 PRELIMINARY; PRT; 121 AA.
ID Q9UL96
AC Q9UL96;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035018; AAD56254.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig_1-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13695 MW; D582D450596BDD35 CRC64;

Query Match
Best Local Similarity 56.1%; Score 344.5; DB 4; Length 121;
Matches 68; Conservative 13; Mismatches 32; Indels 3; Gaps 1;

QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWIRPPGKGLWIGYIHSNTYNPSTL 61
DB 66 SVKSRITINPDSIKQFSLQNLNSVTPEDTAAYVYCARDELGLQGFYWGQGLTVTVSS 122
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DB 6 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWIRPPGKGLWIGYIHSNTYNPSTL 65
QY 62 KSRVTMSVDTSKHFSLRLSVTAADTAAYVYCAR---SDGTLDMNGGTLVTVSS 114
DB 66 KSRITITKDTSKNOVDLTFMTPMDPATYATYCAHRKSGDGYFDYWGQGLTVTVSS 121

RESULT 14
Q99NG4 PRELIMINARY; PRT; 121 AA.
ID Q99NG4
AC Q99NG4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Plasmid PHEN1.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=98169018; PubMed=9510199;
RA Hawlich H., Frank R., Hennecke M., Baensch M., Sohne B., Arseniev L.,
RA Baetsch W., Kola A., Kios A., Koehl J.;
RT "Site-directed C3a-Receptor Antibodies from Phage Display Libraries.";
RL J. Immunol. 160:2947-2958(1998).
DR EMBL; AJ222590; CAA10890.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig_1-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Plasmid.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13255 MW; D293E4B8C859D5B CRC64;

Query Match
Best Local Similarity 55.4%; Score 340; DB 11; Length 121;
Matches 68; Conservative 16; Mismatches 27; Indels 6; Gaps 2;

QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWIRPPGKGLWIGYIHSNTYNPSTL 61
DB 6 ESGPGLVPSQTLSTCTVSGFPLTSHGV--SWVRQPPGKGLWIGYIWDGDKTKYHSAL 63

QY 62 KSRVTMSVDTSKHFSLRLSVTAADTAAYVYCAR---DGYTLDMNGGTLVTVSS 114
DB 64 ISRLSISKDMSKQVFLKLSLQTEPDATYATYCAHRYKANYAMDYWGQGSTVTVSS 120

RESULT 15
Q91X92 PRELIMINARY; PRT; 482 AA.
ID Q91X92
AC Q91X92;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Unknown (Protein for WGC:18822).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011181; AAH11181.1; -.
DR InterPro; IPR007110; Ig_1-like.
```


XX 11-JUL-2002.
 PD 27-DEC-2001; 2001WO-SE02908.
 XX 29-DEC-2000; 2000SE-0004892.
 XX (PHMA) PHARMACIA DIAGNOSTICS AB.
 PA Flicker S, Steindberger P, Kraft D, Valenta R;
 PI Flicker S, Steindberger P, Kraft D, Valenta R;
 DR WPI; 2002-583604/62.
 XX N-PSDB; ABK89639.
 PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for
 PT environmental allergen detection -
 XX
 XX Disclosure; Page 36; 45pp; English.
 PS
 CC This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IgE Fabs and methods for their use. The proteins
 CC of the invention may have antiallergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's
 CC IgE antibodies to Phl p 2 (a major timothy grass pollen allergen).
 CC The group 2 allergen-specific Fabs of the invention may be useful for
 CC environmental allergen detection and for standardisation of allergen
 CC extracts. The Fabs - or a vaccine against a type I allergy is useful for
 CC passive immunotherapy of type I allergy. It is also useful for
 CC diagnosing a type I allergy. The allergen-specific Fabs of the invention
 CC are useful for inter alia, diagnosis, therapy and prevention of type
 CC I allergy. They are also useful for identification of group 2
 CC allergen-containing pollen and may be used for blocking the binding of
 CC grass pollen allergic patients IgE antibodies to Phl p 2. The present
 CC sequence represents the human IgG fab, clone 100 heavy chain protein of
 CC the invention.
 XX
 SO Sequence 114 AA;
 Query Match 98.5%; Score 605; DB 23; Length 114;
 Best Local Similarity 99.1%; Pred. No. 1.4e-44;
 Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LESGPELVKPSQTLSTCTVSGSIRSGYVSWIRPCKGLKEMIGYIHSGNTYYNS 60
 DB 1 LESGPELVKPSQTLSTCTVSGSIRSGYVSWIRPCKGLKEMIGYIHSGNTYYNS 60
 QY 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAIVYVCARSDGYTLDMWGGTLVTYSS 114
 DB 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAIVYVCARSDGYTLDMWGGTLVTYSS 114
 RESULT 2
 ABG30446
 ID ABG30446 standard; Protein; 114 AA.
 XX
 AC ABG30446;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human IgE Fab clone 60 heavy chain protein.
 XX
 KW Human; fab; antiallergic; vaccine; grass pollen; Phl p 2;
 XX timothy grass pollen allergen; passive immunotherapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..26
 FT /note= "FRI region"
 FT 27..33
 FT /note= "CDRI region"

FT Region 34..47
 FT /note= "FR2 region"
 FT Region 48..63
 FT /note= "CDR2 protein"
 FT Region 64..95
 FT /note= "FR3 region"
 FT Region 96..103
 FT /note= "CDR2 region"
 FT Region 104..114
 FT /note= "FR4 region"
 XX
 XX WO200253595-A1.
 XX
 PD 11-JUL-2002.
 XX
 PF 27-DEC-2001; 2001WO-SE02908.
 XX
 PR 29-DEC-2000; 2000SE-0004892.
 XX
 XX (PHMA) PHARMACIA DIAGNOSTICS AB.
 PA Flicker S, Steindberger P, Kraft D, Valenta R;
 PI Flicker S, Steindberger P, Kraft D, Valenta R;
 DR WPI; 2002-583604/62.
 XX N-PSDB; ABK89638.
 XX
 PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for
 PT environmental allergen detection -
 XX
 XX Disclosure; Page 37; 45pp; English.
 PS
 CC This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IgE Fabs and methods for their use. The proteins
 CC of the invention may have antiallergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's
 CC IgE antibodies to Phl p 2 (a major timothy grass pollen allergen).
 CC The group 2 allergen-specific Fabs of the invention may be useful for
 CC environmental allergen detection and for standardisation of allergen
 CC extracts. The Fabs - or a vaccine against a type I allergy is useful for
 CC passive immunotherapy of type I allergy. It is also useful for
 CC diagnosing a type I allergy. The allergen-specific Fabs of the invention
 CC are useful for inter alia, diagnosis, therapy and prevention of type
 CC I allergy. They are also useful for identification of group 2
 CC allergen-containing pollen and may be used for blocking the binding of
 CC grass pollen allergic patients IgE antibodies to Phl p 2. The present
 CC sequence represents the human IgG fab, clone 60 heavy chain protein of
 CC the invention.
 XX
 SO Sequence 114 AA;
 Query Match 97.7%; Score 600; DB 23; Length 114;
 Best Local Similarity 96.5%; Pred. No. 3.8e-44;
 Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LESGPELVKPSQTLSTCTVSGSIRSGYVSWIRPCKGLKEMIGYIHSGNTYYNS 60
 DB 1 LESGPELVKPSQTLSTCTVSGSIRSGYVSWIRPCKGLKEMIGYIHSGNTYYNS 60
 QY 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAIVYVCARSDGYTLDMWGGTLVTYSS 114
 DB 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAIVYVCARSDGYTLDMWGGTLVTYSS 114
 RESULT 3
 ABG30445
 ID ABG30445 standard; Protein; 114 AA.
 XX
 AC ABG30445;
 XX
 DT 21-OCT-2002 (first entry)
 XX

Human IGE Fab clone 94 heavy chain protein.

Human; fab; anti allergic; vaccine; grass pollen; Phi p 2;
timothy grass pollen allergen; passive immunotherapy.

Homo sapiens.

Key	Location/Qualifiers
Region	1..26 /note= "FR1 region"
Region	27..33 /note= "CDR1 region"
Region	34..47 /note= "FR2 region"
Region	48..63 /note= "CDR2 protein"
Region	64..95 /note= "FR3 region"
Region	96..103 /note= "CDR2 region"
Region	104..114 /note= "FR4 region"

WO200253595-A1.
11-JUL-2002.
27-DEC-2001; 2001WO-S02908.
29-DEC-2000; 2000SE-0004892.
(PHAA) PHARMACIA DIAGNOSTICS AB.
Flicker S, Steinberger P, Kraft D, Valenta R;
WPI: 2002-583604/62.
N-PADB; ABR89637.

Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising variable region of group 2 allergen specific-human IGE Fabs, useful for diagnosing or passive immunotherapy of type I allergy, for environmental allergen detection -

Disclosure; Page 36; 45pp; English.

This invention relates to the DNA and protein sequences of group 2 allergen-specific human IGE Fabs and methods for their use. The proteins of the invention may have antiallergic activities and may be used as a vaccine or an inhibitor of binding of grass pollen allergic patient's IgE antibodies to Phi p 2 (a major timothy grass pollen allergen). The group 2 allergen-specific fabs of the invention may be useful for environmental allergen detection and for standardisation of allergen extracts. The fabs - or a vaccine against a type I allergy is useful for passive immunotherapy of type I allergy; it is also useful for diagnosing a type I allergy. The allergen-specific fabs of the invention are useful for inter alia, diagnosis, therapy and prevention of type I allergy. They are also useful for identification of group 2 allergen-containing pollen and may be used for blocking the binding of grass pollen allergic patients IgE antibodies to Phi p 2. The present sequence represents the human IgG fab, clone 94 heavy chain protein of the invention.

Sequence 114 AA;

Query Match 90.6%; Score 556; DB 23; Length 114;
Best Local Similarity 90.4%; Pred. NO. 2.2e-40;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

1 LESGGGLVKKPSQTLISLCTVSGGSIRSGGYWSWIROPKGLLEWIGYIHSGNTYNP 60
1 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
1 LESGGGLVKKPQTLSLSCAVSGSIRSGGYTWSWIROPKGLLEWIGYIHSNTYNP 60
1 LKSRTVMSVDTSKRHFSRLSSVTADTAAYVCARSDGTYLDNNQGTVLTIVSS 114

Db	61	LKSRIMASVDTSEKFSLRINLSVTAAADTAAYYYCARLDGTLTDIGQGLTVTVSS	114
		RESULT 4	
		AAAB36206	
		AAAB36206 standard; protein; 473 AA.	
xx		AAAB36206;	
AC			
xx		15-FEB-2001 (first entry)	
DT			
xx		Human immune system associated protein HISAP-4.	
DE			
xx		Human; immune system associated protein; HISAP-4; immune disorder;	
KM		Infection; autoimmune disease; cancer.	
xx			
OS		Homo sapiens.	
xx			
PN		US6135941-A.	
xx			
PD		24-OCT-2000.	
xx			
PF		27-MAR-1998; 98US-0049672.	
xx			
PR		27-MAR-1998; 98US-0049672.	
xx			
PA		(INCY-) INCYTE PHARM INC.	
xx			
PI		Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn NR;	
PI		Hillman JL, Au-Young J;	
xx		WPI; 2001-030926/04.	
DR		N-PSDB; AAC66522.	
xx			
PT		New human immune system associated proteins (HISAP) and polynucleotides	
PT		encoding the HISAP, useful for diagnosing, treating or preventing	
PT		immune or cell proliferative disorders or infections	
xx			
PS		Claim 1; Column 53-56; 54pp; English.	
xx			
CC		The present invention provides the coding and protein sequences for a	
CC		number of human immune system associated proteins (HISAPs). These can be	
CC		used in the diagnosis and treatment of various autoimmune disorders,	
CC		infections and cell proliferation diseases. The diseases include AIDS,	
CC		adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,	
CC		Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia	
CC		gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus	
CC		erythematosus, arteriosclerosis, cirrhosis and cancer.	
xx			
SO		Sequence 473 AA;	
		Query Match 84.9%; Score 521; DB 22; Length 473;	
		Best Local Similarity 83.2%; Pred. No. 9,8e-37;	
		Matches 99; Conservative 6; Mismatches 8; Indels 6; Gaps 1;	
Oy		2 ESGGGLVYKPSGCTLSLCTVSGSGIRSGGYMSWIRPPKGLKLEWIGYIYHSGNTYINPSL 61	
Db		25 ESGGGLVYKPSGCTLSLCTVSGSGIRSGGYMSWIRPPKGLKLEWIGYIYHSGNTYINPSL 84	
Oy		62 KSRRTMSVDTSEKFSLRINLSVTAAADTAAYYYCARSD-----GYTLDMWGQGLTVTVSS 114	
Db		85 KSRRTISVDTSEKFSLRINLSVTAAADTAAYYYCARDDVGLRGNGYMDWGQGLTVTVSS 143	
		RESULT 5	
		AAAW78433	
		AAAW78433 standard; Protein; 123 AA.	
xx			
AC		AAW78433;	
xx			
DT		11-MAY-1999 (first entry)	


```
OS Homo sapiens.
XX WO200100678-A1.
XX
XX 04-JAN-2001.
XX
XX 23-JUN-2000; 2000WO-US17327.
XX
XX 30-JUN-1999; 99US-0141701.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wackins BA, Reitz MS;
XX
XX WPI; 2001-112438/12.
XX
XX N-PSDB; AAF29076.
XX
XX Novel human monoclonal antibody immunoreactive with human
XX immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
XX in biological sample and providing passive immunotherapy to HIV-1
XX infected mammal
XX
XX PS Claim 1; Page 69; 81pp; English.
XX
XX The present invention provides the protein and coding sequences for the
XX variable regions of human monoclonal antibodies which are immunoreactive
XX with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
XX These can be used in diagnosis and therapy of HIV-1 infection.
XX
XX Sequence 120 AA;
XX
XX Query Match 83.6%; Score 513.5; DB 22; Length 120;
XX Best Local Similarity 86.2%; Pred. No. 1e-36;
XX Matches 100; Conservative 5; Mismatches 6; Indels 5; Gaps 2;
XX
Qy 2 ESGPGLVPSQTLSTCTWVGSGSIRSGGYWMIROPKGLWIGYIHSGNTYYPSTL 61
Db 7 ESGPGLVPSQTLSTCTWVGSGSIRSGGYWMIROPKGLWIGYIHSGNTYYPSTL 66
Qy 62 KSRVTMSVDTSKNHFSRLSSVTADTAAYVYCARS---DGYTLDMWGQGLVTVSS 114
Db 67 KSRVTISVDTSKNHFSRLSSVTADTAAYVYCARGVVDWF--DWMGQGLVTVSS 120

RESULT 8
AAB62745
ID AAB62745 standard; Protein; 123 AA.
XX
XX AAB62745;
XX
XX 03-APR-2001 (first entry)
XX
XX Human HIV-1 monoclonal antibody SEQ ID NO: 44.
XX
XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
XX envelope glycoprotein; gp120; diagnosis.
XX
XX Homo sapiens.
XX
XX WO200100678-A1.
XX
XX 04-JAN-2001.
XX
XX 23-JUN-2000; 2000WO-US17327.
XX
XX 30-JUN-1999; 99US-0141701.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wackins BA, Reitz MS;
XX
XX WPI; 2001-112438/12.
XX
XX N-PSDB; AAF29046.
```

```
XX
XX Novel human monoclonal antibody immunoreactive with human
XX immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
XX in biological sample and providing passive immunotherapy to HIV-1
XX infected mammal
XX
XX PS Claim 1; Page 50; 81pp; English.
XX
XX The present invention provides the protein and coding sequences for the
XX variable regions of human monoclonal antibodies which are immunoreactive
XX with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
XX These can be used in diagnosis and therapy of HIV-1 infection.
XX
XX Sequence 123 AA;
XX
XX Query Match 83.4%; Score 512; DB 22; Length 123;
XX Best Local Similarity 83.8%; Pred. No. 1.4e-36;
XX Matches 98; Conservative 7; Mismatches 8; Indels 4; Gaps 1;
XX
Qy 2 ESGPGLVPSQTLSTCTWVGSGSIRSGGYWMIROPKGLWIGYIHSGNTYYPSTL 61
Db 7 ESGPGLVPSQTLSTCTWVGSGSIRSGGYWMIROPKGLWIGYIHSGNTYYPSTL 66
Qy 62 KSRVTMSVDTSKNHFSRLSSVTADTAAYVYCARS---DGYTLDMWGQGLVTVSS 114
Db 67 KSRVTISVDTSKNHFSRLSSVTADTAAYVYCARGVVDWF--DWMGQGLVTVSS 123

RESULT 9
AAB62765
ID AAB62765 standard; Protein; 122 AA.
XX
XX AAB62765;
XX
XX 03-APR-2001 (first entry)
XX
XX Human HIV-1 monoclonal antibody SEQ ID NO: 64.
XX
XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
XX envelope glycoprotein; gp120; diagnosis.
XX
XX Homo sapiens.
XX
XX WO200100678-A1.
XX
XX 04-JAN-2001.
XX
XX 23-JUN-2000; 2000WO-US17327.
XX
XX 30-JUN-1999; 99US-0141701.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wackins BA, Reitz MS;
XX
XX WPI; 2001-112438/12.
XX
XX N-PSDB; AAF29066.
XX
XX Novel human monoclonal antibody immunoreactive with human
XX immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
XX in biological sample and providing passive immunotherapy to HIV-1
XX infected mammal
XX
XX PS Claim 1; Page 63; 81pp; English.
XX
XX The present invention provides the protein and coding sequences for the
XX variable regions of human monoclonal antibodies which are immunoreactive
XX with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
XX These can be used in diagnosis and therapy of HIV-1 infection.
XX
XX Sequence 122 AA;
XX
XX Query Match 83.1%; Score 510.5; DB 22; Length 122;
```

Best Local Similarity 85.3%; Pred. No. 1.9e-36;
Matches 99; Conservative 5; Mismatches 9; Indels 3; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPGKLEWIGIYHSGNTYNNPSL 61
DB 7 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPGKLEWIGIYHSGNTYNNPSL 66
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARSDGYTLDDNGGGLTVTVSS 114
DB 67 KSRVTISVDTSKNQFSLKLSVTAAADTAAYVYCARMDLRDSTGLCTWGRGLTVTVSS 122

RESULT 10

AA15126
ID AA15126 standard; Protein; 246 AA.

XX AC AA15126;
XX DT 07-FEB-2000 (first entry)
XX DE Anti-murine CTLA-4 M3 sFv.
XX KM Anti-murine CTLA-4 sFv; M3 sFv; single chain antibody; murine CTLA4;
XX KM membrane-associated protein; chimeric construct; extracellular domain;
XX KM human CD8; ligand; activated T-cell; co-stimulatory signal; donor B7;
XX KM recipient CD28; T-cell proliferation;
XX KM xenograft-specific immunosuppression.
XX OS Mus sp.
XX OS Synthetic.
XX PN MO9957266-A2.
XX PD 11-NOV-1999.
XX PF 30-APR-1999; 99MO-GB01350.
XX PR 30-APR-1998; 98GB-0009280.

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX PI Lechler IR, Dörfling A;
XX DR MPI: 2000-038815/03.
XX DR N-PSDB; AA228998.

PT Inhibiting T-cell mediated rejection of xenotransplanted organs

PS Claim 9; Fig 11; 43pp; English.

XX The present sequence is the anti-murine CTLA-4 sFv (M3 sFv). This is a
XX membrane-associated protein which binds to CTLA-4. Chimeric constructs
XX comprising DNA sequences encoding the extracellular domain of murine
XX CTLA4 and human CD8 were used for the study of anti-CTLA4-sFv protein.
XX The anti-CTLA4 sFv functions as a ligand binding to CTLA-4 on activated
XX T-cells and antagonises the co-stimulatory signal provided by the
XX interaction between donor B7 and recipient CD28. Cells expressing the
XX anti-CTLA4 sFv failed to stimulate T-cell proliferation. This is used in
XX xenograft-specific immunosuppression.

SO Sequence 246 AA;

Query Match 83.1%; Score 510; DB 21; Length 246;

Best Local Similarity 85.0%; Pred. No. 4.3e-36;
Matches 96; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPGKLEWIGIYHSGNTYNNPSL 61
DB 8 ESGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPGKLEWIGIYHSGNTYNNPSL 67
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARSDGYTLDDNGGGLTVTVSS 114
DB 68 KSRVTISVDTSKNQFSLKLSVTAAADTAAYVYCARMDLRDSTGLCTWGRGLTVTVSS 120

RESULT 11

AA93713
ID AA93713 standard; Protein; 172 AA.

XX AA93713;

XX DT 03-OCT-2000 (first entry)

XX DE The heavy chain of immunoglobulin clone 2.1.3.

XX KM Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
XX KM hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
XX KM proliferative disorder; cancer; immunodeficient disorder.

XX OS Homo sapiens.

XX PN WO200037504-A2.

XX PD 29-JUN-2000.

XX PF 23-DEC-1999; 99MO-US30895.

XX PR 23-DEC-1998; 98US-0113647.

XX PA (PFIZ) PFIZER INC.
XX PA (ABGE-) ABGENIX INC.

XX PI Hanson DC, Neveu MJ, Mueller EG, Hanke JH, Gilman SC, Davis CG;
XX PI Corvalan JR;

XX DR MPI: 2000-442647/38.

XX DR N-PSDB; AAA46876.

PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
PT (CTLA)-4 containing specified heavy and light chain sequences, useful
PT for treating, e.g. immune disorders -

PS Claim 2; Fig 1G; 157pp; English.

XX The present sequence represents a heavy chain of an antibody of the
XX invention. The antibody is directed cytotoxic T-lymphocyte antigen
XX (CTLA)-4. Antibodies of the invention are composed of a heavy chain
XX variable region, comprising a modified contiguous sequence from a
XX FRI-PR3 sequence encoded by a human VH3-33 family gene. The
XX modifications are contained in CDR1, CDR2 and/or framework regions.
XX The antibodies may be used to inhibit CTLA-4 and down-regulate the
XX immune system to treat hyperimmunity disorders (e.g. autoimmune
XX disease, diabetes and graft rejection) and proliferative disorders
XX (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
XX immune system to up-regulate immunodeficient disorders.

SO Sequence 172 AA;

Query Match 82.7%; Score 508; DB 21; Length 172;

Best Local Similarity 85.1%; Pred. No. 4.4e-36;
Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

QY 3 SGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPGKLEWIGIYHSGNTYNNPSL 62
DB 1 SGPGLVKPSQTLSTCTVSGGSIIRSGGYWMIROPGKLEWIGIYHSGNTYNNPSL 60
QY 63 SRVTMSVDTSKNHFSLRLSSVTAAADTAAYVYCARSDGYTLDDNGGGLTVTVSS 114
DB 61 SRVTISVDTSKNQFSLKLSVTAAADTAAYVYCARSDGYTDVWGGGLTVTVSS 114

RESULT 12

AA30584
ID AA30584 standard; Protein; 126 AA.

XX AA30584;


```

XX 19-MAR-2001 (first entry)
DT A human variable heavy chain region of anti-IgE antibody.
XX
DE Anti-idiotype antibody; C-epsilon3 region; immunoglobulin E; IgE;
XX anti-IgE antibody; mimobody; vaccine; allergy; asthma; atopic dermatitis;
XX rhinitis; chronic urticaria; food allergy; IgE-mediated disease;
XX passive immunisation.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 30..37
XX /note= "complementarity determining region 1"
XX Region 51..67
XX /note= "complementarity determining region 2"
XX Region 100..115
XX /note= "complementarity determining region 3"
XX
XX WO200063252-A1.
XX
XX 26-OCT-2000.
XX
XX 12-APR-2000; 2000WO-BP03288.
XX
XX 14-APR-1999; 99GB-0008533.
XX
XX (NOVS ) NOVARTIS AG.
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Kricek F, Stadler B, Vogel M;
XX
XX WPI; 2000-687161/67.
XX N-PSDB; AAC62336.
XX
XX Novel anti-idiotypic antibody against antibodies which inhibit binding
XX of immunoglobulin E to its high affinity receptor, useful in vaccines
XX for treating diseases such as allergy, rhinitis, atopic dermatitis -
XX
XX Claim 4; Fig 5c; 73pp; English.
XX
XX The present sequence represents a human variable heavy chain region of
XX an anti-idiotype antibody that interferes with the binding of the
XX C-epsilon3 region of immunoglobulin (Ig)E to the high affinity receptor
XX for IgE, i.e. and anti-IgE antibody. Such an antibody is referred to
XX as a mimobody. The anti-IgE antibody fragment is used as a vaccine, and
XX as a pharmaceutical for treating IgE-mediated diseases such as allergy,
XX in particular asthma, atopic dermatitis, rhinitis, chronic urticaria and
XX food allergies. It is also used to treat IgE-mediated diseases. It is
XX also used for raising polyclonal or monoclonal antibodies. The polyclonal
XX or monoclonal antibodies obtained are useful for treating IgE-mediated
XX diseases by passive immunisation.
XX
XX Sequence 126 AA:
SQ

```

Query Match 82.6%; Score 507; DB 21; Length 126;
 Best Local Similarity 80.3%; Pred. No. 3.9e-36;
 Matches 98; Conservative 6; Mismatches 10; Indels 8; Gaps 1;

```

QY 1 LESGGLVKSPTSLTCTVSGGSIIRSGYMSWIRPGKGLMWIGIYHSGNTYNNPS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 5 LESGGLVKSPTSLTCTVSGGSIIRSGYMSWIRPGKGLMWIGIYHSGNTYNNPS 64
QY 61 LKSRVTMSVDTSKNFSRLTSSVTAAADTAAYVYCARSDG-----YTLDNMGCGTLVTV 112
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 65 LKSRVTMSVDTSKNFSRLTSSVTAAADTAAYVYCARSDG-----YTLDNMGCGTLVTV 124
QY 113 SS 114
   ||
DB 125 SS 126

```

```

RESULT 13
ABP54970
ID ABP54970 standard; Protein: 126 AA.
XX
XX ABP54970;
XX
XX 14-JAN-2003 (first entry)
DT
XX
XX Anti-idiotypic VH sequence mimicking IgE conformational epitope.
XX
XX Human; IgE; immunoglobulin; antibody; epitope; mimotope;
XX lactic acid bacterium; allergy; vaccine; anti-allergic;
XX dermatological; anti-inflammatory; anti-idiotype.
XX
XX Homo sapiens.
XX
XX EPI239032-A1.
XX
XX 11-SEP-2002.
XX
XX 02-MAR-2001; 2001EP-0105138.
XX
XX 02-MAR-2001; 2001EP-0105138.
XX
XX (NEST ) SOC PROD NESTLE SA.
XX
XX Stadler BM, Vogel M, Germond J, Fritsche R;
XX
XX WPI; 2002-684058/74.
XX
XX New bacterial strain of lactic acid bacterium group, expressing surface
XX polypeptide which contains peptide sequence mimicking at least part of
XX conformational epitope of immunoglobulin E, useful for treating allergy
XX
XX Claim 4; Page 5; 19pp; English.
XX
XX The present invention relates to recombinant strains of lactic
XX acid bacteria that express surface polypeptides containing
XX peptides (mimotopes) or antibody fragments which mimic at least
XX part of a conformational epitope of an IgE molecule. These are
XX used in food and pharmaceutical compositions, in particular
XX vaccines, for the treatment or prevention of an allergic reaction
XX involving IgE, such as rhinitis, atopic dermatitis and erythema.
XX The mimotope peptides or antibody fragments are obtained by
XX screening random peptide and human Fab antibody phage display
XX libraries with an antibody directed to the Fc part of IgE. The
XX present sequence is the protein sequence of an anti-idiotypic Fab
XX heavy chain variable region (VH) sequence mimicking an IgE
XX conformational epitope.
XX
XX Sequence 126 AA:
SQ

```

Query Match 82.6%; Score 507; DB 23; Length 126;
 Best Local Similarity 80.3%; Pred. No. 3.9e-36;
 Matches 98; Conservative 6; Mismatches 10; Indels 8; Gaps 1;

```

QY 1 LESGGLVKSPTSLTCTVSGGSIIRSGYMSWIRPGKGLMWIGIYHSGNTYNNPS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 5 LESGGLVKSPTSLTCTVSGGSIIRSGYMSWIRPGKGLMWIGIYHSGNTYNNPS 64
QY 61 LKSRVTMSVDTSKNFSRLTSSVTAAADTAAYVYCARSDG-----YTLDNMGCGTLVTV 112
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 65 LKSRVTMSVDTSKNFSRLTSSVTAAADTAAYVYCARSDG-----YTLDNMGCGTLVTV 124
QY 113 SS 114
   ||
DB 125 SS 126

```

RESULT 14
 ABG80712
 ID ABG80712 standard; Peptide: 251 AA.

XX ABG80712;
 AC
 XX
 DT 29-NOV-2002 (first entry)
 DE
 XX Amyloid peptide containing an attachment site #2.
 XX
 XX Molecular antigen array; vaccine; antigen; antimicrobial; mutant;
 KM molecular scaffold; amyloid beta; Abeta 1-42; influenza; mutein;
 KM graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;
 KM adult respiratory distress syndrome; ARDS; Crohn's disease;
 KM allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
 KM Grave's disease; systemic lupus erythematosus; osteoporosis;
 KM inflammatory immune disease; myasthenia gravis; multiple sclerosis;
 KM immunoproliferative disease lymphadenopathy; Alzheimer's disease;
 KM angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
 KM rheumatoid arthritis; diabetes; infectious disease; factor Xa;
 KM enterokinase; cysteine-containing linker.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200256907-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 21-JAN-2002; 2002WO-1B00168.
 XX
 PR 19-JAN-2001; 2001US-262379P.
 PR 04-MAY-2001; 2001US-288549P.
 PR 05-OCT-2001; 2001US-32698P.
 PR 07-NOV-2001; 2001US-331045P.
 XX
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA (NOVS) NOVARTIS PHARMA AG.
 PA (MAUR/) MAURER P.
 PA (LECH/) LECHNER F.
 PA (ORTM/) ORTMANN R.
 PA (LUEC/) LUEBEND R.
 PA (STAU/) STAUFENBIEL M.
 PA (FREY/) FREY P.
 XX
 PI Maurer P., Lechner F., Ortmann R., Luecend R., Staufenbiel M., Frey P.;
 PI Renner WA, Bachmann M., Tissot A., Seibel P., Plosek C;
 XX
 DR WPI; 2002-636514/68.
 XX
 PT Molecular antigen array used in the production of vaccines for
 PT infectious diseases -
 XX
 PS Claim 38; Page 227; 418pp; English.
 XX
 CC The invention relates to a composition comprising: (a) a non-natural
 CC molecular scaffold comprising: (i) a core particle selected from:
 CC (1) a core particle of a non-natural origin; and (2) a core particle of
 CC natural origin; and (ii) an organism comprising at least one first
 CC attachment site, where the organism is connected to the core particle by
 CC at least one covalent bond; (b) an antigen or antigenic determinant with
 CC at least one second attachment site, where the antigen or antigenic
 CC determinant is amyloid beta peptide (Abeta 1-42) or its fragment, and
 CC where the second attachment site is selected from: (i) an attachment site
 CC not naturally occurring with the antigen or antigenic determinant; and
 CC (ii) an attachment site naturally occurring with the antigen or
 CC antigenic determinant, where the second attachment site is capable of
 CC association through at least one non-peptide bond to the first attachment
 CC site; and where the antigen or antigenic determinant and the scaffold
 CC interact through the association to form an ordered and repetitive
 CC antigen array. Also included is a process for producing a non-naturally
 CC occurring ordered and repetitive antigen array. The composition is used
 CC in immunisation and as a vaccine for diseases such as influenza,
 CC graft versus host disease, IGE-mediated allergic reactions, anaphylaxis,
 CC adult respiratory distress syndrome (ARDS), Crohn's disease, allergic
 CC asthma, acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's

CC disease, systemic lupus erythematosus, inflammatory immune diseases,
 CC myasthenia gravis, immunoproliferative disease lymphadenopathy,
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's
 CC disease, osteoporosis and infectious diseases. The present sequence is
 CC a modified antigen for use in the array of the invention. The antigen is
 CC modified to possess a cleavage site (enterokinase or factor Xa) and a
 CC cysteine-containing N- or C-terminal linker peptide which serves as the
 CC attachment point to a virus like particle or bacterial protein (the
 CC scaffold protein).
 XX
 SQ Sequence 251 AA;
 XX
 QY Query Match 82.6%; Score 507; DB 23; Length 251;
 QY Best Local Similarity 80.3%; Pred. No. 86-36;
 DB Matches 98; Conservative 6; Mismatches 10; Indels 8; Gaps 1;
 QY 1 LESGRLVYKPSQTLTLCTVSGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNS 60
 QY 20 LESGRLVYKPSQTLTLCTVSGSIRSGGYWTWIRPPGKLEWIGYIYHSGNTYNS 79
 DB 61 LKSRVTMSVDTSKNHFSLRLSSVTADPAVYVCARSDG-----YTLDMNGCGTIVTV 112
 DB 80 LKSRVTMSVDTSKNHFSLRLSSVTADPAVYVCAREBETGLYPPYIYDVGITIVTV 139
 QY 113 SS 114
 QY ||
 DB 140 SS 141
 XX
 RESULT 15
 ABP45983
 ID ABP45983 standard; Protein; 252 AA.
 XX
 AC ABP45983;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv SEQ ID 1994.
 XX
 KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostratic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 OS
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US19110.
 XX
 PR 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX
 DR WPI; 2002-114799/15.
 XX
 PT Antidodies against B lymphocyte stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX
 PS Claim 1; Page 2779-2780; 3148pp; English.
 XX

CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cyostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.

XX
 SQ Sequence 252 AA;

Query Match 82.6%; Score 507; DB 23; Length 252;
 Best Local Similarity 81.5%; Pred. No. 8e-36;
 Matches 97; Conservative 6; Mismatches 10; Indels 6; Gaps 1;

Oy 2 ESGGLVPSQTLSTCTVSGSIRSGYVWSWIRQPKGLEWIGYTHSGNTYYNPSL 61
 |||||
 Db 6 ESGGLVPSQTLSTCTVSGSIRSGYVWSWIRQPKGLEWIGYTHSGNTYYNPSL 65
 |||||
 Oy 62 KSRVMSVDTSKNHFSLRLSSVTADTAIVYCAR-----SDGYTLDMNGQGLVTVSS 114
 |||||
 Db 66 KSRVMSVDTSKNHFSLRLSSVTADTAIVYCARLPDADYGDYGFDMGQGLVTVSS 124

Search completed: February 10, 2004, 18:36:10
 Job time : 35.3727 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:39:30 ; Search time 26.2545 Seconds
(without alignments)
909.160 Million cell updates/sec

Title: US-10-027-725A-9

Perfect score: 614
Sequence: 1 LESGPGLVKPSQTLSTCTV.....RSDGYTLDMGQGLTVTVSS 114

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	614	100.0	114	US-10-027-725A-9	Sequence 9, Appli
2	600	97.7	114	US-10-027-725A-8	Sequence 8, Appli
3	556	90.6	114	US-10-027-725A-7	Sequence 7, Appli
4	524.5	85.4	121	US-10-309-762-152	Sequence 152, App
5	524	85.3	118	US-10-309-762-138	Sequence 138, App
6	523.5	85.3	123	US-10-309-762-10	Sequence 10, Appl
7	521	84.9	120	US-10-309-762-13	Sequence 13, Appl
8	521	84.9	120	US-10-309-762-144	Sequence 144, App
9	521	84.9	122	US-10-309-762-147	Sequence 147, App
10	520	84.7	221	US-09-972-656-80	Sequence 80, Appl
11	519.5	84.6	121	US-10-309-762-151	Sequence 151, App
12	519.5	84.6	125	US-10-309-762-11	Sequence 11, Appl
13	517.5	84.3	119	US-10-309-762-140	Sequence 140, App
14	516.5	84.1	123	US-10-309-762-12	Sequence 12, Appl
15	516	84.0	124	US-10-309-762-75	Sequence 75, Appl

16	516	84.0	143	US-10-309-762-96	Sequence 96, Appl
17	515.5	84.0	117	US-10-330-613-13	Sequence 13, Appl
18	515.5	84.0	117	US-10-330-613-13	Sequence 13, Appl
19	514	83.7	120	US-10-309-762-128	Sequence 128, App
20	514	83.7	120	US-10-309-762-139	Sequence 139, App
21	514	83.7	121	US-10-308-817-137	Sequence 137, App
22	513	83.6	116	US-10-309-762-127	Sequence 127, App
23	512.5	83.5	125	US-10-309-762-8	Sequence 8, Appl
24	512.5	83.5	125	US-10-309-762-16	Sequence 16, Appl
25	511.5	83.3	119	US-10-309-762-131	Sequence 131, App
26	511	83.2	110	US-10-309-762-74	Sequence 74, App
27	510.5	83.1	123	US-10-309-762-9	Sequence 9, Appl
28	510.5	83.1	127	US-10-309-762-14	Sequence 14, Appl
29	508.5	82.8	125	US-10-309-762-153	Sequence 153, App
30	508	82.7	172	US-10-153-182-21	Sequence 21, App
31	507.5	82.7	117	US-10-330-613-5	Sequence 5, Appl
32	507.5	82.7	117	US-10-330-530-5	Sequence 5, Appl
33	507.5	82.7	123	US-10-309-762-17	Sequence 17, Appl
34	507	82.6	126	US-09-974-449-6	Sequence 6, Appl
35	507	82.6	252	US-09-880-748-1994	Sequence 1994, App
36	506.5	82.5	251	US-10-309-762-143	Sequence 143, App
37	506.5	82.5	251	US-10-120-414-75	Sequence 75, Appl
38	506.5	82.5	253	US-09-880-748-1619	Sequence 1619, App
39	505.5	82.3	123	US-10-309-762-18	Sequence 18, Appl
40	505.5	82.3	123	US-10-309-762-19	Sequence 19, Appl
41	503	81.9	252	US-09-880-748-1329	Sequence 1329, App
42	502.5	81.8	119	US-10-025-687-5	Sequence 5, Appl
43	502.5	81.8	119	US-10-125-687-5	Sequence 5, Appl
44	502	81.8	118	US-10-078-7578-52	Sequence 52, Appl
45	501	81.6	256	US-09-880-748-1607	Sequence 1607, App

ALIGNMENTS

RESULT 1
US-10-027-725A-9
Sequence 9, Application US/10027725A
Publication No. US20030082659A1
GENERAL INFORMATION:
APPLICANT: Flicker, Sabine
TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
FILE REFERENCE: 25401.4
CURRENT FILING DATE: 2002-08-09
CURRENT APPLICATION NUMBER: US/10/027,725A
PRIOR APPLICATION NUMBER: US 60/259,436
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-027-725A-9

Query Match 100.0%; Score 614; DB 15; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.6e-45;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTCTVSGGSIRSGGYWMSWIRPGKLEWIGYIYHSGNTYVPS 60
DB 1 LESGPGLVKPSQTLSTCTVSGGSIRSGGYWMSWIRPGKLEWIGYIYHSGNTYVPS 60
QY 61 LKSRVTMSVDTSKNHFSLRSSVTAADTAAYVVCARSDGYTLDMGQGLTVTVSS 114
DB 61 LKSRVTMSVDTSKNHFSLRSSVTAADTAAYVVCARSDGYTLDMGQGLTVTVSS 114
RESULT 2
US-10-027-725A-8
Sequence 8, Application US/10027725A
Publication No. US20030082659A1
GENERAL INFORMATION:

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; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-8

Query Match          97.7%; Score 600; DB 15; Length 114;
Best Local Similarity 96.5%; Pred. No. 8,8e-48;
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTCTVSGGSIIRSGYWMIRQPEKGLWIGIYHSGNTYNNPS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 LESGPGLVKPSQTLSTCTVSGGSIIRSGYWMIRQPEKGLWIGIYHSGNTYNNPS 60

QY 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114

RESULT 3
US-10-027-725A-7
; Sequence 7, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-7

Query Match          90.6%; Score 556; DB 15; Length 114;
Best Local Similarity 90.4%; Pred. No. 9,6e-44;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 LESGPGLVKPSQTLSTCTVSGGSIIRSGYWMIRQPEKGLWIGIYHSGNTYNNPS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 LESGPGLVKPSQTLSTCTVSGGSIIRSGYWMIRQPEKGLWIGIYHSGNTYNNPS 60

QY 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114

RESULT 4
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
```

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; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-152

Query Match          85.4%; Score 524.5; DB 12; Length 121;
Best Local Similarity 86.2%; Pred. No. 8e-41;
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGYWMIRQPEKGLWIGIYHSGNTYNNPSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 6 ESGPGLVKPSQTLSTCTVSGGSIIRSGYWMIRQPEKGLWIGIYHSGNTYNNPSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 66 KSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114

RESULT 5
US-10-309-762-138
; Sequence 138, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-138

Query Match          85.3%; Score 524; DB 12; Length 118;
Best Local Similarity 88.5%; Pred. No. 8,6e-41;
Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 ESGPGLVKPSQTLSTCTVSGGSIIRSGYWMIRQPEKGLWIGIYHSGNTYNNPSL 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 6 ESGPGLVKPSQTLSTCTVSGGSIIRSGYWMIRQPEKGLWIGIYHSGNTYNNPSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 66 KSRVTMSVDTSKNHFSLRLSVTAADTAVYYCARSDGYTLDMWGQGLTVTVSS 114

RESULT 6
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
```

10 TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IN

TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma

; TITLE OF INVENTION: Neutralizing Activity

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FILE REFERENCE: A-799
CURRENT APPLICATION NUMBER: US/09/972.656
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
SEQ ID NO 80
LENGTH: 221
TYPE: PRT
ORGANISM: Homo sapiens
US-09-972-656-80
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Query Match      84.7%; Score 520; DB 11; Length 221;
Best Local Similarity 86.7%; Pred. No. 3.8e-40;
Matches 98; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
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QY 2 ESGPGLVKSQTLSTLCTVSGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNNPSL 61
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DB 6 ESGPGLVKSQTLSTLCTVSGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNNPSL 65
    |||||
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSPGCTLDNMGCGTLVTYSS 114
    |||||
DB 66 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARSGDWGTFDYWGCGTLVTYSS 118
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RESULT 11
US-10-309-762-151
Sequence 151, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 151
LENGTH: 121
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-151
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Query Match      84.6%; Score 519.5; DB 12; Length 121;
Best Local Similarity 86.2%; Pred. No. 2.3e-40;
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;
```

```
QY 2 ESGPGLVKSQTLSTLCTVSGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNNPSL 61
    |||||
DB 6 ESGPGLVKSQTLSTLCTVSGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNNPSL 65
    |||||
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSD--DGYTLDNMGCGTLVTYSS 114
    |||||
DB 66 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARVLLMFGYGDVWGCGTLVTYSS 121
    |||||
```

```
RESULT 12
US-10-309-762-11
Sequence 11, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
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CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-11
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Query Match      84.6%; Score 519.5; DB 12; Length 125;
Best Local Similarity 83.3%; Pred. No. 2.4e-40;
Matches 100; Conservative 6; Mismatches 7; Indels 7; Gaps 2;
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```
QY 2 ESGPGLVKSQTLSTLCTVSGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNNPSL 61
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DB 6 ESGPGLVKSQTLSTLCTVSGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNNPSL 65
    |||||
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSD---DGY--TLDNMGCGTLVTYSS 114
    |||||
DB 66 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARFYDFLTGYPDAFDMGCGTLVTYSS 125
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```

```
RESULT 13
US-10-309-762-140
Sequence 140, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 140
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-140
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```
Query Match      84.3%; Score 517.5; DB 12; Length 119;
Best Local Similarity 86.8%; Pred. No. 3.4e-40;
Matches 99; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
```

```
QY 2 ESGPGLVKSQTLSTLCTVSGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNNPSL 61
    |||||
DB 6 ESGPGLVKSQTLSTLCTVSGSIRSGYWSWIRPPGKLEWIGYIYHSGNTYNNPSL 65
    |||||
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAAADTAVYYCARSD-GYTLNMGCGTLVTYSS 114
    |||||
DB 66 KSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARGNYYGDMVWGCGTLVTYSS 119
    |||||
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```
RESULT 14
US-10-309-762-12
Sequence 12, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
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FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 12
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-12

Query Match 84.1%; Score 516.5; DB 12; Length 123;
Best Local Similarity 83.9%; Pred. No. 4,4e-40;
Matches 99; Conservative 5; Mismatches 9; Indels 5; Gaps 1;

Oy 2 ESGPGLVPSQTLSTCTVSGGSIIRSGYWSMIRQPPKGLIEWIGYIYHSGNTYYNPSL 61
Db 6 ESGPGLVPSQTLSTCTVSGGSIIRSGYWSMIRQPPKGLIEWIGYIYHSGNTYYNPSL 65
Oy 62 KSRVTMSYDTSKNHPSLRSLSSVTADTAIVYCCAR----SDGYTLDNWGQGLTVTVSS 114
Db 66 KSRVTISYDTSKNQPSLRSLSSVTADTAIVYCCARVTLWFGEDYGYDVWVGQGLTVTVSS 123

RESULT 15

US-10-309-762-75
Sequence 75, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 75
LENGTH: 124
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-75

Query Match 84.0%; Score 516; DB 12; Length 124;
Best Local Similarity 84.0%; Pred. No. 4,9e-40;
Matches 100; Conservative 6; Mismatches 7; Indels 6; Gaps 2;

Oy 2 ESGPGLVPSQTLSTCTVSGGSIIRSGYWSMIRQPPKGLIEWIGYIYHSGNTYYNPSL 61
Db 6 ESGPGLVPSQTLSTCTVSGGSIIRSGYWSMIRQPPKGLIEWIGYIYHSGNTYYNPSL 65
Oy 62 KSRVTMSYDTSKNHPSLRSLSSVTADTAIVYCCARSD----GYT-LDNWGQGLTVTVSS 114
Db 66 KSRVTISYDTSKNQPSLRSLSSVTADTAIVYCCARSDYTLWFGEDYGYDVWVGQGLTVTVSS 124

Search completed: February 10, 2004, 19:03:03
Job time : 27.2545 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:32:44 ; Search time 11.7455 Seconds
(without alignments)
410.664 Million cell updates/sec

Title: US-10-027-725A-9
Perfect score: 614
Sequence: 1 LESRPLGVKPSQTLSTCTV.....RSDGTYLDNMGQGLVTVSS 114

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/6C_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	521	84.9	473	3	US-09-049-672A-4 Sequence 4, Appl
2	502.5	81.8	119	4	US-09-025-769B-39 Sequence 39, Appl
3	502.5	81.8	119	4	US-09-025-769B-65 Sequence 65, Appl
4	496	80.8	122	1	US-08-360-125-11 Sequence 11, Appl
5	496	80.8	122	2	US-08-450-578-11 Sequence 11, Appl
6	496	80.8	122	2	US-09-017-628-11 Sequence 11, Appl
7	496	80.8	122	2	US-09-014-880-11 Sequence 11, Appl
8	496	80.8	122	4	US-08-450-363-11 Sequence 11, Appl
9	491	80.0	118	4	US-09-025-769B-25 Sequence 25, Appl
10	487.5	79.4	119	1	US-08-360-125-5 Sequence 5, Appl
11	487.5	79.4	119	2	US-08-450-578-5 Sequence 5, Appl
12	487.5	79.4	119	2	US-09-017-628-5 Sequence 5, Appl
13	487.5	79.4	119	2	US-09-014-880-5 Sequence 5, Appl
14	487.5	79.4	119	4	US-08-450-363-5 Sequence 5, Appl
15	472	76.9	244	4	US-08-918-148-79 Sequence 79, Appl
16	467	76.1	118	3	US-08-545-809A-116 Sequence 116, Appl
17	466.5	76.0	142	2	US-08-480-774A-2 Sequence 2, Appl
18	463.5	75.5	250	4	US-10-039-785-50 Sequence 50, Appl
19	460.5	75.0	119	2	US-08-652-816A-10 Sequence 10, Appl
20	460	74.9	278	3	US-09-260-527-3 Sequence 3, Appl
21	457	74.4	118	3	US-08-545-809A-142 Sequence 142, Appl
22	457	74.4	118	3	US-09-343-698-6 Sequence 6, Appl
23	450.5	73.4	219	4	US-09-460-384-37 Sequence 37, Appl
24	450	73.3	832	3	US-08-630-820-7 Sequence 7, Appl
25	449	73.1	126	1	US-08-276-852-142 Sequence 142, Appl
26	449	73.1	126	1	US-08-899-575-142 Sequence 142, Appl
27	449	73.1	126	1	US-08-899-575-142 Sequence 142, Appl

28	449	73.1	126	5	PCT-US95-08743-142	Sequence 142, App
29	448	73.0	118	3	US-08-545-809A-123	Sequence 123, App
30	446.5	72.7	98	1	US-08-478-039-75	Sequence 75, Appl
31	446.5	72.7	98	1	US-08-478-349A-75	Sequence 75, Appl
32	446.5	72.7	123	1	US-08-137-117D-64	Sequence 64, Appl
33	446.5	72.7	123	2	US-08-436-717-64	Sequence 64, Appl
34	446.5	72.7	123	4	US-08-793-450-4	Sequence 4, Appl
35	446.5	72.7	138	1	US-08-137-117D-69	Sequence 69, Appl
36	446.5	72.7	138	2	US-08-436-717-69	Sequence 69, Appl
37	446.5	72.7	472	4	US-08-793-450-8	Sequence 8, Appl
38	444	72.3	150	4	US-09-582-337-14	Sequence 14, Appl
39	442.5	72.1	124	1	US-08-478-039-78	Sequence 78, Appl
40	442.5	72.1	124	1	US-08-478-349A-78	Sequence 78, Appl
41	440	71.7	116	3	US-08-545-809A-140	Sequence 140, Appl
42	439.5	71.6	476	3	US-08-487-550-12	Sequence 12, Appl
43	439.5	71.6	476	4	US-09-526-028-12	Sequence 12, Appl
44	439	71.5	244	4	US-10-039-785-44	Sequence 44, Appl
45	435	70.8	120	4	US-08-057-430A-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-049-672A-4
Sequence 4, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Yang, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049, 672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANCUT01

CLONE: 1513264
US-09-049-672A-4

Query Match 84.9%; Score 521; DB 3; Length 473;
Best Local Similarity 83.2%; Pred. No. 1.3e-44;
Matches 99; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

QY 2 EESGPGLVKRSQTLSTLCYVSGGSIKSGYWSWIRQPPKGLWIGYIHSGNTYNNPSL 61
DB 25 EESGPGLVKRSQTLSTLCYVSGGSIKSGYWSWIRQPPKGLWIGYIHSGNTYNNPSL 84
QY 62 KSRVTISVTSKNGFSLRLSSVTADTAAYYCARSD-----GYTLDMNGGGLTVTVSS 114
DB 85 KSRVTISVTSKNGFSLRLSSVTADTAAYYCARSDVGLRGVGMGWGGLTVTVSS 143

RESULT 2
US-09-025-769B-39
Sequence 39, Application US/09025769B

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-39

Query Match 81.8%; Score 502.5; DB 4; Length 119;
Best Local Similarity 85.3%; Pred. No. 1.8e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 EESGPGLVKRSQTLSTLCYVSGGSIKSGYWSWIRQPPKGLWIGYIHSGNTYNNPSL 61
DB 6 EESGPGLVKRSQTLSTLCYVSGGSIKSGYWSWIRQPPKGLWIGYIHSGNTYNNPSL 63
QY 62 KSRVTISVTSKNGFSLRLSSVTADTAAYYCAR--SDG-YTLDMNGGGLTVTVSS 114
DB 62 KSRVTISVTSKNGFSLRLSSVTADTAAYYCAR--SDG-YTLDMNGGGLTVTVSS 114

DB 64 KSRVTISVTSKNGFSLRLSSVTADTAAYYCARWGDGFYAMDYGGLTVTVSS 119

RESULT 3
US-09-025-769B-65
Sequence 65, Application US/09025769B
Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-65

Query Match 81.8%; Score 502.5; DB 4; Length 119;
Best Local Similarity 85.3%; Pred. No. 1.8e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

QY 2 EESGPGLVKRSQTLSTLCYVSGGSIKSGYWSWIRQPPKGLWIGYIHSGNTYNNPSL 61
DB 6 EESGPGLVKRSQTLSTLCYVSGGSIKSGYWSWIRQPPKGLWIGYIHSGNTYNNPSL 63
QY 62 KSRVTISVTSKNGFSLRLSSVTADTAAYYCAR--SDG-YTLDMNGGGLTVTVSS 114
DB 64 KSRVTISVTSKNGFSLRLSSVTADTAAYYCARWGDGFYAMDYGGLTVTVSS 119

RESULT 4
US-08-360-125-11

Sequence 11, Application US/08360125
Patent No. 5767246

GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246hiko ITO
APPLICANT: Kazuhiko NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody

TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:

FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-11
Query Match 80.8%; Score 496; DB 1; Length 122;
Best Local Similarity 81.2%; Pred. No. 8.3e-43;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;
QY 2 ESGPGLVKKPSGTLSTLTCTVSGGSRSGGYKSWTIRBPBGKLEWIGYIHSGNTYVNSPL 61
DB 6 ESGGLVKKPSSTLTCTVSGGSRSGGYSISSYWGIRBPBGKLEWIGYIHSGNTYVNSPL 65
QY 62 KSRVTMSVDTSKINFSLRLSSVTADTAIVYVCARSD----GYLDNNQGQGLTVYSS 114
DB 66 KSRVTISVDTSKINFSLRLSSVTADTAIVYVCARSGTGGYIGNDVWGQGLTVYSS 122
RESULT 5
US-08-450-578-11
Sequence 11, Application US/08450578
Patent No. 5837845
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845hiko ITO
APPLICANT: Kazuhito NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:

ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-11

Query Match 80.8%; Score 496; DB 2; Length 122;
Best Local Similarity 81.2%; Pred. No. 8.3e-43;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

QY 2 ESGPGLVKSQSLTSLCTVSGGSIRSGYWSMIRPPGKGLWIGIYHSNTYNNPSL 61
DB 6 ESGPGLVKSQSLTSLCTVSGGSIRSGYWSMIRPPGKGLWIGIYHSNTYNNPSL 65
QY 62 KSRVTMSVDTSKNHFSLRISVTADTAIVYCARSD---GYLDNMGQGLTVVSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTADTAIVYCARSGSYGGYGMVWGQGLTVVSS 122

RESULT 6
US-09-017-628-11
Sequence 11, Application US/09017628
Patent No. 5990287
GENERAL INFORMATION:
APPLICANT: HOSOKAWA, Saiko
APPLICANT: TAGAWA, Toshiaki
APPLICANT: HIRAKAWA, Yoko
APPLICANT: ITO, No. 5990287/hiko
APPLICANT: NAGAIKE, Kazuhito
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
FILE REFERENCE: 177/527361KH
CURRENT APPLICATION NUMBER: US/09/017,628
EARLIER FILING DATE: 1998-02-02
EARLIER APPLICATION NUMBER: 08/360,135
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 122
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody 1-3-1

US-09-017-628-11

Query Match 80.8%; Score 496; DB 2; Length 122;
Best Local Similarity 81.2%; Pred. No. 8.3e-43;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

QY 2 ESGPGLVKSQSLTSLCTVSGGSIRSGYWSMIRPPGKGLWIGIYHSNTYNNPSL 61
DB 6 ESGPGLVKSQSLTSLCTVSGGSIRSGYWSMIRPPGKGLWIGIYHSNTYNNPSL 65
QY 62 KSRVTMSVDTSKNHFSLRISVTADTAIVYCARSD---GYLDNMGQGLTVVSS 114
DB 66 KSRVTISVDTSKNQFSLKLSVTADTAIVYCARSGSYGGYGMVWGQGLTVVSS 122

RESULT 7
US-09-014-880-11
Sequence 11, Application US/09014880
Patent No. 5990297
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-11
Query Match 80.8%; Score 496; DB 2; Length 122;
Best Local Similarity 81.2%; Pred. No. 8.3e-43;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;
QY 2 ESGPGLVKSQSLTSLCTVSGGSIRSGYWSMIRPPGKGLWIGIYHSNTYNNPSL 61

Db 6 ESQPLVPSKPSLTLCTVSGSGSISSSSYWGMIRQPPGKLEWIGSIYSGSTYNSL 65
QY 62 KSRVTMSVDTSKNHSRLSSVTADTVAVYYCARSD---GYTLDNWGQGLVTVSS 114
66 KSRVTISVDTSKNPSLKLSSVTADTVAVYYCARSGYGGYYGMDVMWGQGLVTVSS 122

RESULT 8

US-08-450-363-11
Sequence 11, Application US/08450363
Patent No. 6436434
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 6436434Ihiko ITO
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C. U.S.A.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,363
FILING DATE: May 25, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHEetical: protein
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLAR:
IMMEDIATE SOURCE:

LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-11

Query Match 80.8% Score 496; DB 4; Length 122;

Best Local Similarity 81.2% Pred. No. 8.3e-43; Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

QY 2 ESQPLVPSKPSLTLCTVSGSGSISSSSYWGMIRQPPGKLEWIGSIYSGSTYNSL 61
Db 6 ESQPLVPSKPSLTLCTVSGSGSISSSSYWGMIRQPPGKLEWIGSIYSGSTYNSL 65
QY 62 KSRVTMSVDTSKNHSRLSSVTADTVAVYYCARSD---GYTLDNWGQGLVTVSS 114
Db 66 KSRVTISVDTSKNPSLKLSSVTADTVAVYYCARSGYGGYYGMDVMWGQGLVTVSS 122

RESULT 9

US-09-025-769B-25
Sequence 25, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knapik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11a5, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-25

Query Match 80.0%; Score 491; DB 4; Length 118;
Best local Similarity 84.3%; Pred. No. 2,5e-42;
Matches 97; Conservative 4; Mismatches 10; Indels 4; Gaps 2;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYMSWIRPPGKLEWIGIYHSGNTYNSPL 61
DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYMSWIRPPGKLEWIGIYHSGNTYNSPL 63
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCA--RSDGTLNNKGGTLVTYSS 114
DB 64 KSRVTISVDTSKNHFSLRLSSVTAADTAVYYCARGGGGGVFDYWGQGLVTYSS 118

RESULT 10

US-08-360-125-5
Sequence 5, Application US/08360125
Patent No. 5767246

GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246hiko ITO
APPLICANT: Kazuhiko NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

US-08-360-125-5

Query Match 79.4%; Score 487.5; DB 1; Length 119;
Best local Similarity 81.6%; Pred. No. 5,8e-42;
Matches 93; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGYMSWIRPPGKLEWIGIYHSGNTYNSPL 61
DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGYMSWIRPPGKLEWIGIYHSGNTYNSPL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTAADTAVYYCARSDGT--LNNKGGTLVTYSS 114
DB 66 KSRVTISVDTSKNHFSLRLSSVTAADTAVYYCARSTRLRGADYWGQGLVTYSS 118

RESULT 11

US-08-450-578-5
Sequence 5, Application US/08450578
Patent No. 5837845

GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845hiko ITO
APPLICANT: Kazuhiko NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA: 578
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL LINE: antibody GAH
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-5

Query Match 79.4%; Score 487.5; DB 2; Length 119;
Best Local Similarity 81.6%; Pred. No. 5,8e-42;
Matches 93; Conservative 10; Mismatches 10; Indels 1; Gaps 1;
QY 2 ESGPGLVPSQTLSTCTVSGSGSIRSGYWSWIRPPGKLEWIGYIYSGNTYNSL 61
DB 6 ESGPGLVPSQTLSTCTVSGSGSISCGFYNNWIRHPGKLEWIGYIYSGSTYNSL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADPVAVYVCARSDGYT-LDNNQGGTLTVSS 114
DB 66 KSRVTISLDTSKSPSLKSLSLTAADTAIVYICANSTRLRGADYWGQGTMTVSS 119
RESULT 12
US-09-017-628-5
Sequence 5, Application US/09017628
Patent No. 5990287
GENERAL INFORMATION:
APPLICANT: HOSOKAWA, Saiko
APPLICANT: TAGAWA, Toshiaki
APPLICANT: HIRAKAWA, Yoko
APPLICANT: ITO, No. 5990287hiko
APPLICANT: NAGAIKE, Kazuhito
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
FILE REFERENCE: 177/527361KH
CURRENT APPLICATION NUMBER: US/09/017,628
CURRENT FILING DATE: 1998-02-02
EARLIER APPLICATION NUMBER: 08/360,125
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 119
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-5
Query Match 79.4%; Score 487.5; DB 2; Length 119;
Best Local Similarity 81.6%; Pred. No. 5,8e-42;
Matches 93; Conservative 10; Mismatches 10; Indels 1; Gaps 1;
QY 2 ESGPGLVPSQTLSTCTVSGSGSIRSGYWSWIRPPGKLEWIGYIYSGNTYNSL 61
DB 6 ESGPGLVPSQTLSTCTVSGSGSISCGFYNNWIRHPGKLEWIGYIYSGSTYNSL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADPVAVYVCARSDGYT-LDNNQGGTLTVSS 114
DB 66 KSRVTISLDTSKSPSLKSLSLTAADTAIVYICANSTRLRGADYWGQGTMTVSS 119
RESULT 13
US-09-014-880-5
Sequence 5, Application US/09014880
Patent No. 5990297
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS

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XX 11-JUL-2002.
 PD
 XX 27-DEC-2001; 2001WO-SE02908.
 PF
 XX 29-DEC-2000; 2000SE-0004892.
 PR
 XX (PHMA) PHARMACIA DIAGNOSTICS AB.
 PA
 PI Flicker S, Steindberger P, Kraft D, Valenta R;
 DR WPI; 2002-583604/62.
 DR N-PSDB; ABRK9640.
 XX
 XX Group 2 allergen-specific immunoglobulin (Ig) E Fabs or IgG comprising
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for
 PT environmental allergen detection -
 PS
 XX Disclosure; Page 39; 45pp; English.
 XX
 CC This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IgE Fabs and methods for their use. The proteins
 CC of the invention may have antiallergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergen patient's
 CC IgE antibodies to Phl p 2 (a major timothy grass pollen allergen).
 CC The group 2 allergen-specific Fabs of the invention may be useful for
 CC environmental allergen detection and for standardisation of allergen
 CC extracts. The Fabs - or a vaccine against a type I allergy is useful for
 CC passive immunotherapy of type I allergy, it is also useful for
 CC diagnosing a type I allergy. The allergen-specific Fabs of the invention
 CC are useful for inter alia, diagnosis, therapy and prevention of type
 CC I allergy. They are also useful for identification of group 2
 CC allergen-containing pollen and may be used for blocking the binding of
 CC grass pollen allergen patient's IgE antibodies to Phl p 2. The present
 CC sequence represents the human IgG fab, clone 94 light chain protein of
 CC the invention.
 CC
 SQ Sequence 106 AA;
 Query Match 98.2%; Score 533; DB 23; Length 106;
 Best Local Similarity 99.1%; Pred. No. 2.2e-33;
 Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EITQSPSSLSASVGRVTITSCRASQRIINTYLNWYQHKRGPAPKLIYAASSLSQGVPSRF 60
 DB 1 EITQSPSSLSASVGRVTITSCRASQRIINTYLNWYQHKRGPAPKLIYAASSLSQGVPSRF 60
 QY 61 SSGSGGTDFTLTITSSLOFEDFASVYCOESLSASVTFGGGTKEIKR 106
 DB 61 SSGSGGTDFTLTITSSLOFEDFASVYCOESLSASVTFGGGTKEIKR 106
 RESULT 2
 AAR54260
 ID AAR54260 standard; protein; 107 AA.
 AC AAR54260;
 XX
 DT 25-MAR-2003 (updated)
 DT 10-NOV-1994 (first entry)
 XX
 DE Anti-HIV gp120 immunoglobulin light chain variable region b22.
 XX
 XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KW neutralisation; monoclonal antibody; kappa light chain;
 KW variable region; framework; complementarity determining region.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 1..21
 FT Region
 FT /label= FRI

FT Region 22..33
 FT /label= CDR1
 FT Region 34..48
 FT /label= FR2
 FT Region 49..55
 FT /label= CDR2
 FT Region 56..87
 FT /label= FR3
 FT Region 88..95
 FT /label= CDR3
 FT Region 96..107
 FT /label= FR4
 PN
 XX WO9407922-A1.
 XX
 PD 14-APR-1994.
 XX
 XX 30-SEP-1993; 93US-WO09328.
 PF
 XX 30-SEP-1992; 92US-0954148.
 PR
 XX (SCRI) SCRIPPS RES INST.
 PA
 PI Barbas CF, Burton DR, Lerner RA;
 XX
 DR WPI; 1994-135516/16.
 XX
 PT New human monoclonal antibodies neutralising HIV - react with
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
 PT or in vitro diagnosis and for passive immuno-therapy
 PS
 XX Claim 5; Page 189; 248pp; English.
 XX
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E.coli XL1
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the Mab regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VK region sequence AAR54260 neutralises HIV1
 CC gp120.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 107 AA;
 Query Match 87.5%; Score 475; DB 15; Length 107;
 Best Local Similarity 87.7%; Pred. No. 5.4e-29;
 Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
 QY 1 EITQSPSSLSASVGRVTITSCRASQRIINTYLNWYQHKRGPAPKLIYAASSLSQGVPSRF 60
 DB 1 EITQSPSSLSASVGRVTITSCRASQRIINTYLNWYQHKRGPAPKLIYAASSLSQGVPSRF 60
 QY 61 SSGSGGTDFTLTITSSLOFEDFASVYCOESLSASVTFGGGTKEIKR 106
 DB 61 SSGSGGTDFTLTITSSLOFEDFASVYCOESLSASVTFGGGTKEIKR 106
 RESULT 3
 AAM01283
 ID AAM01283 standard; Protein; 107 AA.
 AC AAM01283;
 XX
 DT 29-JAN-1997 (first entry)
 DT
 XX
 DE VL region of HIV neutralising Mab, clone b22 and B35.
 XX
 XX Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW Mab; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.

XX	OS	Homo sapiens.
XX	FH	Key
XX	FT	Region
XX	FT	/label= FR1
XX	FT	1..21
XX	FT	22..32
XX	FT	/label= CDR1
XX	FT	33..47
XX	FT	/label= FR2
XX	FT	48..54
XX	FT	/label= CDR2
XX	FT	55..86
XX	FT	/label= FR3
XX	FT	87..95
XX	FT	/label= CDR3
XX	FT	96..107
XX	FT	/label= FR4
XX	PN	MO9602273-AI.
XX	PD	01-FEB-1996.
XX	PF	11-JUL-1995;
XX	PR	95WO-US08743.
XX	PA	18-JUN-1994; 94US-0276852.
XX	PS	(SCRI) SCRIPPS RES INST.
XX	PI	Barbas CF, Burton DR, Lerner RA;
XX	PT	WPI; 1996-179601/18.
XX	PT	Monoclonal antibody binding to VI/V2 loop of HIV gp120 - used in
XX	PT	passive immuno:therapy and detection of HIV infection.
XX	PS	Example; Fig 11; 366bp; English.
CC	CC	The sequences given in AAW01261-92 represent the light chain variable
CC	CC	regions (VL) of a series of monoclonal antibodies (Mab's) which are
CC	CC	immunoreactive with HIV glycoprotein gp120 and are capable of
CC	CC	neutralising HIV. This sequence represents the sequence of the JK2
CC	CC	gene clones, b22 and B35. A Mab containing this VL sequence has the
CC	CC	capacity to reduce HIV infectivity titre in an in vivo virus
CC	CC	infectivity assay by 50 % at a concentration of less than 700 ng
CC	CC	of antibody/ml, and binds mature gp120 preferentially over the
CC	CC	precursor gp160. The Mab may be used for determining immunocompetence
CC	CC	of a human anti-HIV antibody and in the detection of HIV infection.
XX	SQ	Sequence 107 AA:
XX	Query Match	87.5%; Score 475; DB 17; Length 107;
XX	Best Local Similarity	87.7%; Pred. No. 5.4e-29;
XX	Matches 93; Conservative	6; Mismatches 7; Indels 0; Gaps 0
OY	1	ELTGSPPSSLSASVGDGVITISCRASGRINTLYNMVQHKGKAPKLLIYAASSLQGSPSRF 60
DB	1	ELTGSPSSLSASVGDGVITICRASQSISSYLNMYOQKGGKAPKLIIYAASSLQGVPSRF 60
OY	61	SGSGGTGDTLTILSLQEPDPAAYCYCOESLSASTFFCGCTKEIKR 106
DB	61	SGSGGTGDTLTILSLQEPDAFYVCOSYSTPYTFGGGTKEIKR 106
RESULT 4		
ID	AA95135	standard; Protein, 107 AA.
AC	AA95135;	
DC	30-JUN-2000	(first entry)
DE	Anti-gp120 antibody light chain variable region from clone b22.	

[illegible]

XX 04-JUL-2000 (first entry)
 DE Anti-gp120 antibody light chain variable region from clone b22.
 XX
 KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.
 XX
 OS Homo sapiens.
 XX
 PN AU9948754-A.
 XX
 PD 17-FEB-2000.
 XX
 PF 16-SEP-1999; 99AU-0048754.
 XX
 PR 16-SEP-1999; 99AU-0048754.
 XX
 PA (SCRI) SCRIpps RES INST.
 XX
 PI Burton DR, Barbas CF, Lerner RA;
 XX
 DR WPI; 2000-246867/22.
 XX
 PT Human neutralizing monoclonal antibodies to human immunodeficiency
 XX virus (HIV) used for providing passive immunotherapy to HIV are
 XX specific for glycoprotein-120 -
 PS
 XX Example 9; Figure 11; 374pp; English.
 CC This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody
 CC capable of reducing an HIV infectivity titre in an in vitro virus
 CC infectivity assay by 50% at a concentration of less than 70 ng/ml. The
 CC method for the production of the antibody comprises:
 CC (a) providing a first polynucleotide encoding a heavy chain
 CC immunoglobulin amino acid sequence (which does not comprise the sequence
 CC represented by AA998206) and a second polynucleotide encoding a light
 CC chain immunoglobulin amino acid sequence;
 CC (b) inserting the first and second polynucleotide sequences into a host
 CC cell;
 CC (c) maintaining the host cell in conditions which allow the amino acid
 CC sequences encoded by the polynucleotides to be expressed in the host
 CC cell; and
 CC (d) isolating the antibody comprising the heavy and light chain
 CC immunoglobulin amino acid sequences from the host cell.
 CC The anti-HIV gp-120 monoclonal antibody is used for providing passive
 CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used
 CC for neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting
 CC HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the
 CC antibodies associated with monoclonal antibodies of xenogeneic or
 CC chimeric derivation.
 CC
 XX Sequence 107 AA;

Query Match 87.5%; Score 475; DB 21; Length 107;
 Best Local Similarity 87.7%; Pred. No. 5,4e-29;
 Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITISCRASQRIINTYLMWYQHKPKAKPLIYAASSLSQGVPSRF 60
 |||||
 DB 1 ELTQSPSSLSASVGRVITITCARASQSISSYLMWYQKPKAKPLIYAASSLSQGVPSRF 60
 |||||
 QY 61 SSGSGTDFTLTISLSQFEDFASYYCOESLSASTYFGGCTKVEIKR 106
 |||||
 DB 61 SSGSGTDFTLTISLSQFEDFATYVCOOSYSTPYFGGCTKVEIKR 106
 |||||
 RESULT 6
 AAG93667
 ID AAG93667 standard; Protein; 107 AA.
 XX
 AC AAG93667;
 XX
 DT 14-SEP-2001 (first entry)
 XX
 DE Human anti-Rh(D) antibody clone SH54 protein sequence.
 XX
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.
 XX
 OS Homo sapiens.
 XX
 PN US6255455-B1.
 XX
 PD 03-JUL-2001.
 XX
 PF 29-JAN-1999; 99US-0240274.
 XX
 PR 11-OCT-1996; 96US-0028550.
 PR 10-APR-1998; 98US-0081380.
 PR 27-JUN-1997; 97US-0884045.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Siegel DL;
 XX
 DR WPI: 2001-388931/41.
 DR N-PADB; AAH68724.
 XX
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine -
 PS Claim 1; Column 70; 162pp; English.
 XX
 CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH6615 to AAH6726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.
 CC
 XX Sequence 107 AA;

Query Match 87.3%; Score 474; DB 22; Length 107;
 Best Local Similarity 87.7%; Pred. No. 6,4e-29;
 Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

DT	14-SEP-2001	(first entry)
XX	AAAG33590	
ID	AAAG33590	standard; Protein; 107 AA.
XX	AAAG33590;	
AC	AAAG33590;	
XX	AAAG33590;	
DT	14-SEP-2001	(first entry)
XX	14-SEP-2001	(first entry)
DE	Human anti-Rh(D) chain I02 protein sequence.	
XX	Human anti-Rh(D) chain I02 protein sequence.	
KW	Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;	
KW	red blood cell; Rh phenotype; diagnosis; therapeutic.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	US6255455-B1.	
XX	US6255455-B1.	
PD	03-JUL-2001.	
XX	03-JUL-2001.	
PF	29-JAN-1999;	99US-0240274.
XX	29-JAN-1999;	99US-0240274.
PR	11-OCT-1996;	96US-0028550.
XX	11-OCT-1996;	96US-0028550.
PR	10-APR-1998;	98US-0081380.
XX	10-APR-1998;	98US-0081380.
PR	27-JUN-1997;	97US-0084045.
XX	27-JUN-1997;	97US-0084045.
PA	(TYPE-) UNIV PENNSYLVANIA.	
XX	(TYPE-) UNIV PENNSYLVANIA.	
PI	Siegel DL;	
XX	Siegel DL;	
DR	WPI; 2001-388931/41.	
XX	WPI; 2001-388931/41.	
DR	N-PSDB; AAH68647.	
XX	N-PSDB; AAH68647.	
PT	New isolated protein, preferably a human anti-Rh(D) antibody for use in	
PT	diagnostics requiring a human instead of an animal antibody and in	
PT	therapeutic medicine -	
XX	therapeutic medicine -	
PS	Claim 1; Column 43; 162pp; English.	
XX	Claim 1; Column 43; 162pp; English.	
CC	The present invention describes an isolated Rh(D) binding protein,	
CC	preferably a human antibody, (I) having an amino acid sequence comprising	
CC	one of the sequences (S) given in AAAG33558 to AAAG3669. (I) has	
CC	immunostimulant activity, and can be used as an immune system stimulant.	
CC	(I) can be used in diagnostic and therapeutic medicine. The antibodies	
CC	are used in diagnostics that require human antibodies instead of animal	
CC	antibodies, such as determine the Rh phenotype of human red blood cells.	
CC	AAH68615 to AAH68726 represent the nucleotide sequence which encode	
CC	AAAG33558 to AAAG3669. AAAG3670 to AAAG3697 represent anti-Rh(D) heavy	
CC	chain CDR3 amino acid sequences which are given in the exemplification	
CC	of the present invention.	
XX	of the present invention.	
Sequence	107 AA;	
Query Match	86.9%;	Score 472; DB 22; Length 107;
Best Local Similarity	87.7%;	Pred. No. 9e-29;
Matches	93; Conservative	6; Mismatches 7; Indels 0; Gaps 0;
OY	1 ELTQSPSSLSASVGRVTITCSASQRIINTYLMWYQHKRKAPKLLIYAASSIQSGVPSRF	60
DB	2 ELTQSPSSLSASVGRVTITCSASQRIINTYLMWYQHKRKAPKLLIYAASSIQSGVPSRF	61
OY	61 SGGSGTDTFTLLTSSLOFEDFASYCCOESLSASYTFGQGTKEIKR	106
DB	62 SGGSGTDTFTLLTSSLOFEDFASYCCOESLSASYTFGQGTKEIKR	107
RESULT 8		
ID	AAAG33663	
XX	AAAG33663	standard; Protein; 107 AA.
XX	AAAG33663;	
DT	14-SEP-2001	(first entry)

DE	Human anti-Rh(D) antibody clone SH49 protein sequence.	XX
XX		XX
KW	Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;	XX
KW	red blood cell; Rh phenotype; diagnosis; therapeutic.	XX
OS	Homo sapiens.	XX
XX		XX
FN	US6255455-B1.	XX
PD	03-JUL-2001.	XX
XX		XX
PF	29-JAN-1999; 99US-0240274.	XX
XX		XX
PR	11-OCT-1996; 96US-0028550.	XX
PR	10-APR-1998; 98US-0081380.	XX
PR	27-JUN-1997; 97US-0884045.	XX
XX		XX
PA	(VYPE-) UNIV PENNSYLVANIA.	XX
FI	Siegel DL;	XX
XX		XX
DR	WPI; 2001-388931/41.	XX
DR	N-PSDB; AAH68720.	XX
XX		XX
PT	New isolated protein, preferably a human anti-Rh(D) antibody for use in	XX
PT	diagnostics requiring a human instead of an animal antibody and in	XX
PT	therapeutic medicine -	XX
PS	Claim 1; Column 69; 162pp; English.	XX
XX		XX
CC	The present invention describes an isolated Rh(D) binding protein,	XX
CC	preferably a human antibody, (1) having an amino acid sequence comprising	XX
CC	one of the sequences (S) given in AAG93558 to AAG93669. (1) has	XX
CC	immunostimulant activity, and can be used as an immune system stimulant.	XX
CC	(1) can be used in diagnostic and therapeutic medicine. The antibodies	XX
CC	are used in diagnostics that require human antibodies instead of animal	XX
CC	antibodies, such as determine the Rh phenotype of human red blood cells.	XX
CC	AAH6815 to AAH68726 represent the nucleotide sequence which encode	XX
CC	AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy	XX
CC	chain CD33 amino acid sequences which are given in the exemplification	XX
CC	of the present invention.	XX
XX		XX
SQ	Sequence 107 AA;	XX
XX		XX
Query Match	86.9%; Score 472; DB 22; Length 107;	
Best Local Similarity	86.8%; Pred. No. 9e-29;	
Matches 92; Conservative	7; Mismatches 7; Indels 0; Gaps 0	
QY	1 ELTQSPSSLSASVGVDRVITSCASGRINTYLNWTOHKFGKPKLLITYAASSLQSGVPSRF 60	
DB	2 ELTQSPSSLSASVGVDRVITVTCRASQSSISISYLNWYQOKGKAPKLLIYAASSLQSGVPSRF 61	
QY	61 SGGSGYGFDTFTLTSSLPEDFASVYCOQSSLASVYFGGCTVVEIKR 106	
DB	62 SGGSGYGFDTFTLTSSLPEDFATVYCOQSYSTPWFQGTVEIKR 107	
RESULT 9		
AAG93664		
ID	AAG93664 standard; Protein; 107 AA.	
XX		
AC	AAG93664;	
XX		
DT	14-SEP-2001 (first entry)	
XX		
DE	Human anti-Rh(D) antibody clone SH50 protein sequence.	
XX		
XX	Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;	
KW	red blood cell; Rh phenotype; diagnosis; therapeutic.	
OS	Homo sapiens.	
XX		

PN US6255455-B1.
 XX
 PD 03-JUL-2001.
 XX
 PF 29-JAN-1999; 99US-0240274.
 XX
 PR 11-OCT-1996; 96US-0028550.
 PR 10-APR-1998; 98US-0081380.
 PR 27-JUN-1997; 97US-0884045.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Siegel DL;
 XX
 DR MPI: 2001-388931/41.
 DR N-PSDB; AAH68721.
 XX
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine -
 XX
 PS Claim 1; Column 69; 162pp; English.
 XX
 CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH6615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 107 AA;
 XX
 Query Match 86.9%; Score 472; DB 22; Length 107;
 Best Local Similarity 86.8%; Pred. No. 9e-29; Indels 0; Gaps 0;
 Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGRVITSCRASORINTYLMWYQHKGKAPKLLIYAASSLSQGVPSRF 60
 DB 2 ELTQSPSSLSASVGRVITSCRASQSISSYLMWYQKPKAPKLLIYAASSLSQGVPSRF 61
 QY 61 SSGSGYTDFTLTITSSLOFEDFASYYCOESLSASYYTFCGCTKVEIKR 106
 DB 62 SSGSGYTDFTLTITSSLOFEDFATYYCOQSYSTPWFQGTKEIKR 107
 XX
 RESULT 10
 AAG93644
 ID AAG93644 standard; Protein; 107 AA.
 XX
 AC AAG93644;
 XX
 DT 14-SEP-2001 (first entry)
 XX
 DE Human anti-Rh(D) antibody clone SH3 protein sequence.
 XX
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.
 XX
 OS Homo sapiens.
 XX
 PN US6255455-B1.
 XX
 PD 03-JUL-2001.
 XX
 PF 29-JAN-1999; 99US-0240274.
 XX
 PR 11-OCT-1996; 96US-0028550.
 PR 10-APR-1998; 98US-0081380.
 PR 27-JUN-1997; 97US-0884045.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Siegel DL;
 XX
 DR MPI: 2001-388931/41.
 DR N-PSDB; AAH68721.
 XX
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine -
 XX
 PS Claim 1; Column 69; 162pp; English.
 XX
 CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH6615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 107 AA;
 XX
 Query Match 86.7%; Score 471; DB 22; Length 107;
 Best Local Similarity 86.8%; Pred. No. 1.1e-28;
 Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGRVITSCRASORINTYLMWYQHKGKAPKLLIYAASSLSQGVPSRF 60
 DB 2 ELTQSPSSLSASVGRVITSCRASQSISSYLMWYQKPKAPKLLIYAASSLSQGVPSRF 61
 QY 61 SSGSGYTDFTLTITSSLOFEDFASYYCOESLSASYYTFCGCTKVEIKR 106
 DB 62 SSGSGYTDFTLTITSSLOFEDFATYYCOQSYSTPWFQGTKEIKR 107
 XX
 RESULT 11
 AAG93593
 ID AAG93593 standard; Protein; 107 AA.
 XX
 AC AAG93593;
 XX
 DT 14-SEP-2001 (first entry)
 XX
 DE Human anti-Rh(D) chain 105 protein sequence.
 XX
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.
 XX
 OS Homo sapiens.
 XX
 PN US6255455-B1.
 XX
 PD 03-JUL-2001.
 XX
 PF 29-JAN-1999; 99US-0240274.
 XX
 PR 11-OCT-1996; 96US-0028550.
 PR 10-APR-1998; 98US-0081380.
 PR 27-JUN-1997; 97US-0884045.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Siegel DL;
 XX
 DR MPI: 2001-388931/41.
 DR N-PSDB; AAH68650.
 XX

PR 27-JUN-1997; 97US-0884045.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Siegel DL;
 XX
 DR MPI: 2001-388931/41.
 DR N-PSDB; AAH68701.
 XX
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine -
 XX
 PS Claim 1; Column 68; 162pp; English.
 XX
 CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH6615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 107 AA;
 XX
 Query Match 86.7%; Score 471; DB 22; Length 107;
 Best Local Similarity 86.8%; Pred. No. 1.1e-28;
 Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGRVITSCRASORINTYLMWYQHKGKAPKLLIYAASSLSQGVPSRF 60
 DB 2 ELTQSPSSLSASVGRVITSCRASQSISSYLMWYQKPKAPKLLIYAASSLSQGVPSRF 61
 QY 61 SSGSGYTDFTLTITSSLOFEDFASYYCOESLSASYYTFCGCTKVEIKR 106
 DB 62 SSGSGYTDFTLTITSSLOFEDFATYYCOQSYSTPWFQGTKEIKR 107
 XX
 RESULT 11
 AAG93593
 ID AAG93593 standard; Protein; 107 AA.
 XX
 AC AAG93593;
 XX
 DT 14-SEP-2001 (first entry)
 XX
 DE Human anti-Rh(D) chain 105 protein sequence.
 XX
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.
 XX
 OS Homo sapiens.
 XX
 PN US6255455-B1.
 XX
 PD 03-JUL-2001.
 XX
 PF 29-JAN-1999; 99US-0240274.
 XX
 PR 11-OCT-1996; 96US-0028550.
 PR 10-APR-1998; 98US-0081380.
 PR 27-JUN-1997; 97US-0884045.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Siegel DL;
 XX
 DR MPI: 2001-388931/41.
 DR N-PSDB; AAH68650.
 XX

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine -
 XX
 PS Claim 1; Column 44; 162pp; English.
 CC
 CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (1) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (1) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (1) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.
 CC
 XX Sequence 107 AA:
 SO
 Query Match 86.2%; Score 468; DB 22; Length 107;
 Best Local Similarity 86.8%; Pred. No. 1.8e-28;
 Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVTITSCASQRIINTYINWQHKGKAPKLLITVAASLSQGVPSRF 60
 |||||
 DB 2 ELTQSPSSLSASVGRVTITCRASQIRRYLNWYQHKRGKAPKLLITVAASLSQGVPSRF 61
 :|||
 QY 61 SGGSGTDTFTLTITSLQFEDFASYYCOESLSASVTFGGGTVEIKR 106
 :|||
 DB 62 TCGSGGTDTFTLTITSLQFEDFATYYCOGSYSTPTGCGTVEIKR 107
 |||||

RESULT 12
 AAR54261
 ID AAR54261 standard; protein; 107 AA.
 AC AAR54261;
 XX
 DT 25-MAR-2003 (updated)
 DT 10-NOV-1994 (first entry)
 XX
 DE Anti-HIV gp120 immunoglobulin light chain variable region b27.
 XX
 KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
 KW neutralisation; monoclonal antibody; kappa light chain;
 KW variable region; framework; complementarity determining region.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..21
 FT /label= FR1
 FT 22..33
 FT /label= CDR1
 FT 34..48
 FT /label= FR2
 FT 49..55
 FT /label= CDR2
 FT 56..87
 FT /label= FR3
 FT 88..95
 FT /label= CDR3
 FT 96..107
 FT /label= FR4
 XX
 PN WO9407922-A1.
 XX
 PD 14-APR-1994.
 XX
 PF 30-SEP-1993; 93WO-US09328.
 XX

PR 30-SEP-1992; 92US-0954148.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbae CF, Burton DR, Lerner RA;
 XX
 DR WPI; 1994-135516/16.
 XX
 PT New human monoclonal antibodies neutralising HIV - react with
 PT gp120 or gp41 and nucleic acid encoding them, useful for in vivo
 PT or in vitro diagnosis and for passive immuno-therapy
 XX
 PS Claim 5; Page 190; 248pp; English.
 CC
 CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
 CC amplification using primers specific for heavy and light chain
 CC variable regions. The amplification products were inserted into a
 CC dicistronic vector to produce a library of fragments. E.coli XL1
 CC Blue cells were transformed with the library. Filamentous phage were
 CC produced which expressed the MAb regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VK region sequence AAR54261 neutralises HIV1
 CC gp120.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX Sequence 107 AA:
 SO
 Query Match 86.0%; Score 467; DB 15; Length 107;
 Best Local Similarity 86.8%; Pred. No. 2.2e-28;
 Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVTITSCASQRIINTYINWQHKGKAPKLLITVAASLSQGVPSRF 60
 |||||
 DB 1 ELTQSPSSLSASVGRVTITCRASQISISYINWYQKRGKAPKLLITVAASLSQGVPSRF 60
 :|||
 QY 61 SGGSGTDTFTLTITSLQFEDFASYYCOESLSASVTFGGGTVEIKR 106
 :|||
 DB 61 SGGSGTDTFTLTITSLQFEDFATYYCOGSYSTPTGCGTVEIKR 106
 |||||

RESULT 13
 AAM01284
 ID AAM01284 standard; Protein; 107 AA.
 AC AAM01284;
 XX
 DT 29-JAN-1997 (first entry)
 DT
 XX
 DE VL region of HIV neutralising MAb, clone b27.
 XX
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection; HIV infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..21
 FT /label= FR1
 FT 22..32
 FT /label= CDR1
 FT 33..47
 FT /label= FR2
 FT 48..54
 FT /label= CDR2
 FT 55..86
 FT /label= FR3
 FT 87..95
 FT /label= CDR3
 FT 96..107
 FT /label= FR4
 XX
 PN
 PD
 PF
 FT
 FT
 XX

PN MO9602273-A1.
 XX
 PD 01-FEB-1996.
 XX
 PF 11-JUL-1995; 95MO-US08743.
 XX
 PR 18-JUL-1994; 94US-0276852.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Burton DR, Lerner RA;
 XX WPI; 1996-179601/18.
 DR
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 XX passive immunotherapy and detection of HIV infection.
 PS
 XX Example; Fig 11; 366pp; English.
 CC The sequences given in AAM01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (Mab's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JK2
 CC gene clone, b27. A Mab containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay
 CC by 50 % at a concentration of less than 700 ng of antibody/ml, and
 CC binds mature gp120 preferentially over the precursor gp160. The Mab
 CC may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 CC
 SQ Sequence 107 AA;
 Query Match 86.0%; Score 467; DB 17; Length 107;
 Best Local Similarity 86.8%; Pred. No. 2.2e-28;
 Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPKAKPLIYAASSLSQGVPSRF 60
 DB 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPKAKPLIYAASSLSQGVPSRF 60
 QY 61 SSGSGYGTDFLTITSSLOFEDFASYYCQESLSASYTFGQGTKEIKR 106
 DB 61 SSGSGYGTDFLTITSSLOFEDFATYYCQGSYSTPTQTFGQGTKEIKR 106
 RESULT 14
 ID AAY95136
 XX AAY95136 standard; Protein; 107 AA.
 AC AAY95136;
 XX
 DT 30-JUN-2000 (first entry)
 XX
 DE Anti-gp120 antibody light chain variable region from clone B27.
 XX
 KM Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KM reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KM glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
 XX
 OS Homo sapiens.
 XX
 PN AU9948756-A.
 PD 17-FEB-2000.
 XX
 PF 16-SEP-1999; 99AU-0048756.
 XX
 PR 16-SEP-1999; 99AU-0048756.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Burton DR, Barbas CF, Lerner RA;
 XX

DR WPI; 2000-293393/26.
 XX
 XX Novel human monoclonal antibodies which immunoreact with and neutralise
 PT human immunodeficiency virus useful for treating HIV infections -
 XX
 XX Example 9; Figure 11; 366pp; English.
 PS
 XX The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50%, at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV.
 CC
 SQ Sequence 107 AA;
 Query Match 86.0%; Score 467; DB 21; Length 107;
 Best Local Similarity 86.8%; Pred. No. 2.2e-28;
 Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPKAKPLIYAASSLSQGVPSRF 60
 DB 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPKAKPLIYAASSLSQGVPSRF 60
 QY 61 SSGSGYGTDFLTITSSLOFEDFASYYCQESLSASYTFGQGTKEIKR 106
 DB 61 SSGSGYGTDFLTITSSLOFEDFATYYCQGSYSTPTQTFGQGTKEIKR 106
 RESULT 15
 ID AAY98245
 XX AAY98245 standard; Protein; 107 AA.
 AC AAY98245;
 XX
 DT 04-JUL-2000 (first entry)
 XX
 DE Anti-gp120 antibody light chain variable region from clone B27.
 XX
 KM Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KM human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KM passive immunotherapy; reduce severity; HIV-induced disease;
 KM immunocompetence; active immunisation.
 XX
 OS Homo sapiens.
 XX
 PN AU9948754-A.
 PD 17-FEB-2000.
 XX
 PF 16-SEP-1999; 99AU-0048754.
 XX
 PR 16-SEP-1999; 99AU-0048754.
 XX

XX (SCRI) SCRIPPS RES INSTR.

XX PA Burton DR, Barbas CF, Lerner RA;

XX PI WPI; 2000-246867/22.

XX DR
XX PT Human neutralizing monoclonal antibodies to human immunodeficiency
PT virus (HIV) used for providing passive immunotherapy to HIV are
PT specific for glycoprotein-120 .

XX Example 9; Figure 11; 374pp; English.

XX This sequence represents a fragment of the antibodies of the invention.
CC The invention relates to the production of an anti-HIV (human
CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody
CC capable of reducing an HIV infectivity titre in an in vitro virus
CC infectivity assay by 50% at a concentration of less than 70 ng/ml. The
CC method for the production of the antibody comprises:
CC (a) providing a first polynucleotide encoding a heavy chain
CC immunoglobulin amino acid sequence (which does not comprise the sequence
CC represented by AA199206) and a second polynucleotide encoding a light
CC chain immunoglobulin amino acid sequence;
CC (b) inserting the first and second polynucleotide sequences into a host
CC cell;
CC (c) maintaining the host cell in conditions which allow the amino acid
CC sequences encoded by the polynucleotides to be expressed in the host
CC cell; and
CC (d) isolating the antibody comprising the heavy and light chain
CC immunoglobulin amino acid sequences from the host cell.
CC The anti-HIV gp-120 monoclonal antibody is used for providing passive
CC immunotherapy to HIV in a human. They can be administered to high-risk
CC patients to reduce the likelihood and/or severity of HIV-induced disease
CC and to patients who are already HIV-infected. The antibodies are used
CC for neutralising field isolates which provides information about the
CC immunocompetence of an immune response in HIV patients, for detecting
CC HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC producing anti-idiotypic antibodies which can be used for active
CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC reduce the problems of significant host immune response to the
CC antibodies associated with monoclonal antibodies of xenogeneic or
CC chimeric derivation.

XX Sequence 107 AA;

Query Match 86.0%; Score 467; DB 21; Length 107;

Best Local Similarity 86.8%; Pred. No. 2.2e-28;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

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QY 1 ELTOSPSSLSASVGRVITSCASORINTYINMYGHKPKAKLIIYAASSLSQSVPSRF 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 ELTOSPSSLSASVGRVITTCRASQSISSYINMYQKPKAKLIIYAASSLSQSVPSRF 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGSGYGTDTLTLISLQFEDFASYYCOESLSASYTFGGOTKVEIKR 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 SGSGGTDTLTLISLQFEDFATYYCOOSYSPPTFGGOTKVEIKR 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Search completed: February 10, 2004, 18:36:11
Job time : 32.9606 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	543	100.0	106	15	US-10-027-725A-10	Sequence 10, App1
2	475	87.5	107	12	US-10-016-986-104	Sequence 104, App1
3	474	87.3	107	11	US-09-848-798-179	Sequence 179, App1
4	472	86.9	107	11	US-09-848-798-33	Sequence 33, App1
5	472	86.9	107	11	US-09-848-798-175	Sequence 175, App1
6	472	86.9	107	11	US-09-848-798-176	Sequence 176, App1
7	471	86.7	107	11	US-09-848-798-156	Sequence 156, App1
8	468	86.2	107	11	US-09-848-798-36	Sequence 36, App1
9	467	86.0	107	12	US-10-016-986-105	Sequence 105, App1
10	465	85.6	111	12	US-10-203-754A-57	Sequence 57, App1
11	464.5	85.5	108	11	US-09-848-798-32	Sequence 32, App1
12	464.5	85.5	108	11	US-09-848-798-43	Sequence 43, App1
13	464	85.5	107	11	US-09-848-798-37	Sequence 37, App1
14	464	85.5	240	9	US-09-192-854-2	Sequence 2, App1
15	464	85.5	240	10	US-09-968-561A-2	Sequence 2, App1

16	464	85.5	240	12	US-09-968-744A-2	Sequence 2, Appl1
17	463	85.3	107	11	US-09-791-153A-67	Sequence 67, Appl1
18	462	85.1	106	15	US-10-027-725A-12	Sequence 12, Appl1
19	462	85.1	107	11	US-09-848-798-38	Sequence 38, Appl1
20	462	85.1	107	11	US-09-848-798-38	Sequence 39, Appl1
21	461	84.9	107	11	US-09-848-798-158	Sequence 158, Appl1
22	460.5	84.8	108	11	US-09-848-798-167	Sequence 167, Appl1
23	460	84.7	106	15	US-10-027-725A-11	Sequence 11, Appl1
24	459.5	84.6	108	11	US-09-848-798-163	Sequence 163, Appl1
25	458	84.3	107	11	US-09-848-798-35	Sequence 35, Appl1
26	458	84.3	107	11	US-09-848-798-173	Sequence 173, Appl1
27	458	84.3	111	12	US-10-203-754A-55	Sequence 56, Appl1
28	457	84.2	104	12	US-10-016-986-106	Sequence 106, Appl1
29	457	84.2	107	11	US-09-848-798-40	Sequence 40, Appl1
30	457	84.2	214	15	US-10-153-382-19	Sequence 19, Appl1
31	456	84.0	107	11	US-09-848-798-44	Sequence 44, Appl1
32	455	83.8	107	12	US-10-309-762-88	Sequence 88, Appl1
33	452	83.2	107	11	US-09-848-798-172	Sequence 172, Appl1
34	452	83.2	107	11	US-09-848-798-174	Sequence 174, Appl1
35	451.5	83.1	108	11	US-09-848-798-41	Sequence 41, Appl1
36	451.5	83.1	108	12	US-10-016-986-109	Sequence 109, Appl1
37	451.5	83.1	107	11	US-09-848-798-168	Sequence 168, Appl1
38	451	83.1	107	12	US-10-309-762-88	Sequence 88, Appl1
39	450	82.9	107	11	US-09-848-798-34	Sequence 34, Appl1
40	449	82.7	107	11	US-09-848-798-164	Sequence 164, Appl1
41	448	82.5	106	12	US-10-377-121-5	Sequence 5, Appl1
42	448	82.5	107	11	US-09-848-798-162	Sequence 162, Appl1
43	447	82.3	108	9	US-09-056-160B-12	Sequence 12, Appl1
44	447	82.3	108	12	US-10-234-671-12	Sequence 12, Appl1
45	447	82.3	108	12	US-09-795-798-3	Sequence 3, Appl1

ALIGNMENTS

```

RESULT 1
US-10-027-725A-10
:
Sequence 10, Application US/10027725A
Publication No. US20030082559A1
GENERAL INFORMATION:
APPLICANT: Flicker, Sabine
TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
FILE REFERENCE: 25401-4
CURRENT APPLICATION NUMBER: US/10/027,725A
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/259,436
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 106
TYPE: PRT
ORGANISM: Homo sapiens
US-10-027-725A-10

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Query Match          100.0%; Score 543; DB 15; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.2e-44;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ELTQSPSSLSAVCDRYTISCRASORINTNTYNTWYOHKRGKAPKLLIYAASSLSQGVPSRF 60
        |||
DB       1 ELTQSPSSLSAVCDRYTISCRASORINTNTYNTWYOHKRGKAPKLLIYAASSLSQGVPSRF 60
        |||

QY      61 SGSGCYGTFITLITISLQFEDFASYYCCESLSASYTFGGGIVKEIKR 106
        |||
DB       61 SGSGCYGTFITLITISLQFEDFASYYCCESLSASYTFGGGIVKEIKR 106
        |||

RESULT 2
US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:

```

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APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
FILE REFERENCE: 313.2CON1
CURRENT APPLICATION NUMBER: US/10/016,986
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 09/149,898
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: US 08/899,575
PRIOR FILING DATE: 1997-07-24
PRIOR APPLICATION NUMBER: US 08/276,852
PRIOR FILING DATE: 1994-07-18
PRIOR APPLICATION NUMBER: US 08/178,302
PRIOR FILING DATE: 1994-01-06
PRIOR APPLICATION NUMBER: PCT/US93/09328
PRIOR FILING DATE: 1993-09-30
PRIOR APPLICATION NUMBER: US 07/954,148
PRIOR FILING DATE: 1992-09-30
NUMBER OF SEQ ID NOS: 176
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 104
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized
US-10-016-986-104
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Query Match      87.5%; Score 475; DB 12; Length 107;
Best Local Similarity 87.7%; Pred. No. 6,5e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
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QY      1 ELTQSPSSLSASVGDVNTTSCRASQRIINTYLNWYQHKPKAPKLLIYAASSLSQGVPSRF 60
      |||
DB      1 ELTQSPSSLSASVGDVNTTSCRASQSISSYLNWYQKPKAPKLLIYAASSLSQGVPSRF 60
      |||
QY      61 SGGSGYDTFTLTSSLSQFEDFASVYCOESLSASVYFGQGTKEIKR 106
      |||
DB      61 SGGSGGTDFTLTSSLSQFEDFATVYCOOSYSTLTFTFGQGTKEIKR 106
      |||
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RESULT 3
US-09-848-798-179
; Sequence 179, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179
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Query Match      87.3%; Score 474; DB 11; Length 107;
Best Local Similarity 87.7%; Pred. No. 8.1e-38;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
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```
QY      1 ELTQSPSSLSASVGDVNTTSCRASQRIINTYLNWYQHKPKAPKLLIYAASSLSQGVPSRF 60
```

```
DB      2 ELTQSPSSLSASVGDVNTTSCRASQSISSYLNWYQKPKAPKLLIYAASSLSQGVPSRF 61
      |||
QY      61 SGGSGYDTFTLTSSLSQFEDFASVYCOESLSASVYFGQGTKEIKR 106
      |||
DB      62 SGGSGGTDFTLTSSLSQFEDFATVYCOOSYSTLTFTFGQGTKEIKR 107
      |||
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RESULT 4
US-09-848-798-33
; Sequence 33, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-848-798-33
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Query Match      86.9%; Score 472; DB 11; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-37;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
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```
QY      1 ELTQSPSSLSASVGDVNTTSCRASQRIINTYLNWYQHKPKAPKLLIYAASSLSQGVPSRF 60
      |||
DB      2 ELTQSPSSLSASVGDVNTTSCRASQSISSYLNWYQKPKAPKLLIYAASSLSQGVPSRF 61
      |||
QY      61 SGGSGYDTFTLTSSLSQFEDFASVYCOESLSASVYFGQGTKEIKR 106
      |||
DB      62 SGGSGGTDFTLTSSLSQFEDFATVYCOOSYSTLTFTFGQGTKEIKR 107
      |||
```

```
RESULT 5
US-09-848-798-175
; Sequence 175, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175
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```
Query Match      86.9%; Score 472; DB 11; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.3e-37;
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Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Query 1 ELTSPSSLSASVGDRTVITCRASORINTYLMWYOHKRGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTSPSSLSASVGDRTVITCRASQSISSYLMWYQKRGKAPKLLIYAASSLSQGVPSRF 61

Qy 61 SSGSGTDFTLTISLQFEDFASYYCOESLSASTYFGGKTVEIKR 106
Db 62 SSGSGTDFTLTISLQFEDFATYYCOOSYSTPTFGGKTVEIKR 107

RESULT 6
US-09-848-798-176
; Sequence 176, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-848-798-176

Query Match 86.9%; Score 472; DB 11; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.3e-37;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTSPSSLSASVGDRTVITCRASORINTYLMWYOHKRGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTSPSSLSASVGDRTVITCRASQSISSYLMWYQKRGKAPKLLIYAASSLSQGVPSRF 61

Qy 61 SSGSGTDFTLTISLQFEDFASYYCOESLSASTYFGGKTVEIKR 106
Db 62 SSGSGTDFTLTISLQFEDFATYYCOOSYSTPTFGGKTVEIKR 107

RESULT 7
US-09-848-798-156
; Sequence 156, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-156

Query Match 86.7%; Score 471; DB 11; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.6e-37;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTSPSSLSASVGDRTVITCRASORINTYLMWYOHKRGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTSPSSLSASVGDRTVITCRASQSISSYLMWYQKRGKAPKLLIYAASSLSQGVPSRF 61

Qy 61 SSGSGTDFTLTISLQFEDFASYYCOESLSASTYFGGKTVEIKR 106
Db 62 SSGSGTDFTLTISLQFEDFATYYCOOSYSTPTFGGKTVEIKR 107

RESULT 8
US-09-848-798-36
; Sequence 36, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 105
US-09-848-798-36

Query Match 86.2%; Score 468; DB 11; Length 107;
Best Local Similarity 86.8%; Pred. No. 3e-37;
Matches 92; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ELTSPSSLSASVGDRTVITCRASORINTYLMWYOHKRGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTSPSSLSASVGDRTVITCRASQSISSYLMWYQKRGKAPKLLIYAASSLSQGVPSRF 61

Qy 61 SSGSGTDFTLTISLQFEDFASYYCOESLSASTYFGGKTVEIKR 106
Db 62 TGGSGTDFTLTISLQFEDFATYYCOOSYSTPTFGGKTVEIKR 107

RESULT 9
US-10-016-986-105
; Sequence 105, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06

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; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for windows version 4.0
; SEQ ID NO 105
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-105
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Query Match      86.0%; Score 467; DB 12; Length 107;
Best Local Similarity 86.8%; Pred. No. 3.7e-37;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
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QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPKAPKLLIYAASSLSQGVPSRF 60
    |||||
DB 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPKAPKLLIYAASSLSQGVPSRF 60
    |||||
QY 61 SSGSGYDPTLTITSSLOPEDFASYYCOESLSA-SYTFQGTVEIKR 106
    |||||
DB 61 SSGSGYDPTLTITSSLOPEDFATYYCOQSYSTPPTFGQGTLEIKR 106
    |||||
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RESULT 10
US-10-203-754A-57
; Sequence 57, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
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; APPLICANT: ITAMI, Seima
; APPLICANT: SEKI, Makoto
; APPLICANT: MATSUDA, Yoshiharu
; APPLICANT: SHIBUI, Tatsuou
; APPLICANT: YOTSUMOTO, Yoshihisa
; APPLICANT: MIYAMURA, Tatsuou
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-203-754A-57
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Query Match      85.6%; Score 465; DB 12; Length 111;
Best Local Similarity 84.8%; Pred. No. 6e-37;
Matches 89; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
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QY 2 LNTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPKAPKLLIYAASSLSQGVPSRF 61
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DB 4 LNTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPKAPKLLIYAASSLSQGVPSRF 63
    |||||
QY 62 SSGYGTDPFTLTITSSLOPEDFASYYCOESLSA-SYTFQGTVEIKR 106
    |||||
DB 64 SSGSGYDPTLTITSSLOPEDFATYYCOQSYSTPPTFGQGTLEIKR 108
    |||||
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RESULT 11
US-09-848-798-32
; Sequence 32, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
```

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; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 101
US-09-848-798-32
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Query Match      85.5%; Score 464.5; DB 11; Length 108;
Best Local Similarity 86.9%; Pred. No. 6.5e-37;
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;
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QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPKAPKLLIYAASSLSQGVPSRF 60
    |||||
DB 2 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPKAPKLLIYAASSLSQGVPSRF 61
    |||||
QY 61 SSGSGYDPTLTITSSLOPEDFASYYCOESLSA-SYTFQGTVEIKR 106
    |||||
DB 62 SSGSGYDPTLTITSSLOPEDFATYYCOQSYSTPPTFGQGTLEIKR 108
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RESULT 12
US-09-848-798-43
; Sequence 43, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
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; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 112
US-09-848-798-43
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Query Match      85.5%; Score 464.5; DB 11; Length 108;
Best Local Similarity 86.9%; Pred. No. 6.5e-37;
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;
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QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPKAPKLLIYAASSLSQGVPSRF 60
    |||||
DB 2 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLNWYQHKPKAPKLLIYAASSLSQGVPSRF 61
    |||||
QY 61 SSGYGTDPFTLTITSSLOPEDFASYYCOESLSA-SYTFQGTVEIKR 106
    |||||
DB 62 SSGSGYDPTLTITSSLOPEDFATYYCOQSYSTPPTFGQGTLEIKR 108
    |||||
```

```
RESULT 13
US-09-848-798-37
; Sequence 37, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
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APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 106
US-09-848-798-37

Query Match 85.5%; Score 464; DB 11; Length 107;
Best Local Similarity 85.8%; Pred. No. 7.2e-37;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASORINTYINWYQHKPKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITSCRASORINTYINWYQHKPKAPKLLIYAASSLSQGVPSRF 61
Qy 61 SSGSGVDTFTLTISLQEPEDFASYYCOESLSASVTFGGQTKVEIKR 106
Db 62 SSGSGGTDFTLTISLQEPEDFATYYCOQSYSTPNTFGQTKVEIKR 107

RESULT 14
US-09-192-854-2
Sequence 2, Application US/09192854
Patent No. US20020068276A1
GENERAL INFORMATION:
APPLICANT: Winter, Greg
APPLICANT: Tomlinson, Ian
TITLE OF INVENTION: Methods for Selecting Functional Peptides
FILE REFERENCE: 3789/72916
CURRENT APPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-09-192-854-2

Query Match 85.5%; Score 464; DB 9; Length 240;
Best Local Similarity 85.8%; Pred. No. 1.7e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASORINTYINWYQHKPKAPKLLIYAASSLSQGVPSRF 60
Db 135 QMTQSPSSLSASVGDRTVITSCRASORINTYINWYQHKPKAPKLLIYAASSLSQGVPSRF 194
Qy 61 SSGSGVDTFTLTISLQEPEDFASYYCOESLSASVTFGGQTKVEIKR 106
Db 195 SSGSGGTDFTLTISLQEPEDFATYYCOQSYSTPNTFGQTKVEIKR 240

RESULT 15
US-09-968-561A-2
Sequence 2, Application US/09968561A
Patent No. US20020164642A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M

APPLICANT: Winter, Gregory
TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
FILE REFERENCE: 8039/1072B
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/GB98/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/511,939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-09-968-561A-2

Query Match 85.5%; Score 464; DB 10; Length 240;
Best Local Similarity 85.8%; Pred. No. 1.7e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASORINTYINWYQHKPKAPKLLIYAASSLSQGVPSRF 60
Db 135 QMTQSPSSLSASVGDRTVITSCRASORINTYINWYQHKPKAPKLLIYAASSLSQGVPSRF 194
Qy 61 SSGSGVDTFTLTISLQEPEDFASYYCOESLSASVTFGGQTKVEIKR 106
Db 195 SSGSGGTDFTLTISLQEPEDFATYYCOQSYSTPNTFGQTKVEIKR 240

Search completed: February 10, 2004, 19:03:03
Job time : 24.4121 secs

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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:26:58 ; Search time 10.9212 Seconds
(without alignments)
933.402 Million cell updates/sec

Title: US-10-027-725A-10
Perfect score: 543
Sequence: 1 ELTQSPSSLSASVGDRTVTS.....QESLSASYTFGQGTVEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	464	85.5	127	2	S40367 Ig kappa chain V-J
2	459	84.5	123	2	S40331 Ig kappa chain - h
3	458	84.3	108	2	B49047 Ig kappa chain V r
4	456	84.0	108	2	S47182 Ig kappa chain - h
5	452	83.2	109	2	S31979 Ig kappa chain - h
6	452	83.2	109	2	S31998 Ig kappa chain - h
7	448	82.5	109	2	S31980 Ig kappa chain - h
8	446	82.1	108	2	S44122 Ig kappa chain V r
9	445	82.0	109	2	S32001 Ig kappa chain - h
10	441	81.2	108	2	S19674 Ig kappa chain V r
11	439	80.8	109	2	S31981 Ig kappa chain V r
12	439	80.8	129	2	S52793 Ig kappa chain V r
13	438	80.7	107	2	S36264 Ig kappa chain V
14	437	80.5	108	2	S31977 Ig kappa chain - h
15	436	80.3	109	2	S31983 Ig kappa chain - h
16	436	80.3	122	2	S40370 Ig kappa chain - h
17	436	80.3	129	1	K1HDMK Ig kappa chain pre
18	436	80.3	129	2	S40317 Ig kappa chain - h
19	435	80.1	128	2	S46372 Ig light chain var
20	434	79.9	120	2	S46370 Ig kappa chain V-J
21	433.5	79.8	125	2	S40315 Ig kappa chain V-I
22	433	79.7	108	1	K1HDMK Ig kappa chain V-I
23	432	79.6	132	2	S40334 Ig kappa chain - h
24	431	79.4	109	2	S31978 Ig kappa chain - h
25	430	79.2	108	1	K1HDMK Ig kappa chain V-I
26	430	79.2	132	2	S36646 Ig kappa chain V r
27	425	78.3	122	2	S40314 Ig kappa chain - h
28	425	78.3	129	2	S40369 Ig kappa chain - h
29	424.5	78.2	106	2	PC2397 anti-tetanus toxin

30	423.5	78.0	124	2	S40336 Ig kappa chain V-J
31	422.5	77.8	107	2	S36275 Ig lambda chain V
32	422	77.7	125	2	S40333 Ig kappa chain V-J
33	422	77.7	131	2	S40352 Ig kappa chain V-J
34	420	77.3	108	1	K1HDMK Ig kappa chain V-I
35	420	77.3	125	2	S40349 Ig kappa chain V-I
36	420	77.3	126	2	S40350 Ig kappa chain V-J
37	419	77.2	125	2	S40350 Ig kappa chain - h
38	418	77.0	117	2	S46371 Ig kappa chain V-J
39	418	77.0	129	2	S52792 Ig kappa chain V r
40	417	76.8	117	2	S46376 Ig kappa chain V-J
41	416	76.6	108	1	K1HDMK Ig kappa chain V-I
42	414	76.2	107	2	J10139 Ig kappa chain V r
43	414	76.2	107	2	S36262 Ig kappa chain V r
44	414	76.2	108	1	K1HDMK Ig lambda chain V
45	413.5	76.2	108	2	S30521 Ig kappa chain V r

ALIGNMENTS

```
RESULT 1
S40367
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40367
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; PMID:94080891; PMID:8258341
A:Accession: S40367
A>Status: preliminary; translation not shown
A:Residues: 1-127 <KLE>
A:Molecule type: mRNA
A:Cross-references: EMBL:X72477
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match      85.5%; Score 464; DB 2; Length 127;
Best Local Similarity 84.9%; Pred. No. 4e-36;
Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY      1 ELTQSPSSLSASVGDRTVTSGRASQRTNTYNTQHKRGKPKLLIYAASLSQGVPSRF 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      20 QMTQSPSSLSASVGDRTVTCRASQISNTYNTQKRGKPKLLIYAASLSQGVPSRF 79
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      61 SSGSGTDFLTITISLQPEDFASYYCOESLSASYTFGQGTVEIKR 106
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      80 SSGSGTDFLTITISLQPEDFATYYCOOSYNTPTTFGQGTVEIKR 125
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 2
S40331
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40331
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; PMID:94080891; PMID:8258341
A:Accession: S40331
A:Molecule type: mRNA
A>Status: preliminary; translation not shown
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72441; NID:G441350; PIDN:CAA51109.1; PID:G441351
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match      84.5%; Score 459; DB 2; Length 123;
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R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
F:16-90/Domain: immunoglobulin homology <IMM>
A:Accession: S31980
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-109 <POR>
A:Cross-references: EMBL:Z15076; NID:G38491; PIDN:CAA78786.1; PID:G38492; EMBL:Z15083; N
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
Query Match 82.5%; Score 448; DB 2; Length 109;
Best Local Similarity 81.0%; Pred. No. 1e-34;
Matches 85; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
OY 2 LTQSPSSLSASVGVDRVTISCRASORINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRFS 61
Db 4 MTQSPSSLSASVGVDRVTISCRASQNIKYLWYQKPKAPKELLITGTSLQSGVPSRFS 63
OY 62 GSGGCTDFTLTITSLQFEDFASVYCOESLSASVTFGGCTKVEIKR 106
Db 64 GSGGCTDFTLTITSLQFEDFATVYFCQGSYSSPYTFGGCTKLEIKR 108
RESULT 8
S44122
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44122
R:Hawkins, R.E.; Zhu, D.; Owecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable H
A:Reference number: S44105
A:Accession: S44122
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <HAM>
A:Cross-references: EMBL:Z31390; NID:G472976; PIDN:CAA83265.1; PID:G940533
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
Query Match 82.1%; Score 446; DB 2; Length 108;
Best Local Similarity 83.0%; Pred. No. 1.6e-34;
Matches 88; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
OY 1 ELTQSPSSLSASVGVDRVTISCRASORINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRFS 60
Db 3 QMTQSPSSLSASVGVDRVTITCRASQSISSYLMWYQKPKAPKLLIYASASSLSQGVPSRFS 62
OY 61 GSGGCTDFTLTITSLQFEDFASVYCOESLSASVTFGGCTKVEIKR 106
Db 63 GSGGCTDFTLTITSLQFEDFATVYFCQGSYSSPYTFGGCTKVEIKR 108
RESULT 9
S32001
Ig kappa chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S32001
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A:Reference number: S31977
A:Accession: S32001
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-109 <POR>
A:Cross-references: EMBL:Z15082; NID:G38503; PIDN:CAA78791.1; PID:G38504

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
Query Match 82.0%; Score 445; DB 2; Length 109;
Best Local Similarity 80.0%; Pred. No. 1.9e-34;
Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
OY 2 LTQSPSSLSASVGVDRVTISCRASORINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRFS 61
Db 4 MTQSPSSLSASVGVDRVTISCRASQNIKYLWYQKPKAPKELLITGTSLQSGVPSRFS 63
OY 62 GSGGCTDFTLTITSLQFEDFASVYCOESLSASVTFGGCTKVEIKR 106
Db 64 GSGGCTDFTLTITSLQFEDFATVYFCQGSYSSPYTFGGCTKVEIKR 108
RESULT 10
S19674
Ig kappa chain V region (clone alpha-TEL9) - human
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19674
R:Marks, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.
Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A:Reference number: S19663; MUID:92085276; PMID:1748994
A:Accession: S19674
A:Molecule type: mRNA
A:Residues: 1-108 <MAR>
A:Cross-references: EMBL:X61642; NID:G37860; PIDN:CAA43823.1; PID:G1335386
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
Query Match 81.2%; Score 441; DB 2; Length 108;
Best Local Similarity 82.9%; Pred. No. 4.5e-34;
Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
OY 2 LTQSPSSLSASVGVDRVTISCRASORINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRFS 61
Db 4 LTQSPSSLSASVGVDRVTITCRASQSISSYLMWYQKPKAPKLLIYAASLSQGVPSRFS 63
OY 62 GSGGCTDFTLTITSLQFEDFASVYCOESLSASVTFGGCTKVEIKR 106
Db 64 GSGGCTDFTLTITSLQFEDFATVYFCQGSYSSPYTFGGCTKVEIKR 108
RESULT 11
S31981
Ig kappa chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S31981
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A:Reference number: S31977
A:Accession: S31981
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-109 <POR>
A:Cross-references: EMBL:Z15077; NID:G38493; PIDN:CAA78786.1; PID:G38494
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
Query Match 80.8%; Score 439; DB 2; Length 109;
Best Local Similarity 80.0%; Pred. No. 7e-34;
Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
OY 2 LTQSPSSLSASVGVDRVTISCRASORINTYLMWYQHKPGKAPKLLIYAASLSQGVPSRFS 61
Db 4 MTQSPSSLSASVGVDRVTITCRASQSISSYLMWYQKPKAPKELLITGTSLQSGVPSRFS 63

Db 4 MTQSPSSLSASVGDRTVITCRASQDISRYLNMWYQKPKAPKLLIHGASTLESVGPGRFS 63
 QY 62 GSGYGTDFTLTITSSLOPEDFASVYCOESLSASTFGCGTKVEIKR 106
 64 GSGSGTDFLTITSSLOPEDFATVYCOQSYSTPPTFGCGTKLEIKR 108

RESULT 12

S52793
 Ig kappa chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
 C:Accession: S52793
 R:Rocca, A.; Khamilchi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denotoy, L.; Deret, submitted to the EMBL Data Library, March 1995
 A:Description: Light chain V region gene usage restriction and peculiarities in myeloma-
 A:Reference number: S52789
 A:Accession: S52793
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-129 <ROC>
 A:Cross-references: EMBL:X65997; NID:G758600; PIDN:CAA59989.1; PID:G758601
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:18-112/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 439; DB 2; Length 129;
 Best Local Similarity 81.9%; Pred. No. 8.3e-34;
 Matches 86; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQDISRYLNMWYQKPKAPKLLIYAASLSQSGVPSRF 60
 25 QMTQSPSSLSASVGDRTVITCRASQDISRYLNMWYQKPKAPKLLIYAASLSQSGVPSRF 84
 Db 61 GSGYGTDFTLTITSSLOPEDFASVYCOESLSASTFGCGTKVEIKR 105
 85 GSGSGTDFLTITSSLOPEDFATVYCOQSYSTPPTFGCGTKVEIKR 129

RESULT 13

S36264
 Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
 C:Accession: S36264
 R:Griffiths, A.D.; Malngvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.; EMO J. 12, 725-734, 1993
 A>Title: Human anti-self antibodies with high specificity from phage display libraries.
 A:Reference number: S36256; MUID:93178448; PMID:7679990
 A:Accession: S36264
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-107 <GRI>
 A:Cross-references: EMBL:Z18845; NID:G33426; PIDN:CAA79297.1; PID:G939919
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 438; DB 2; Length 107;
 Best Local Similarity 83.7%; Pred. No. 8.5e-34;
 Matches 87; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITCRASQDISRYLNMWYQKPKAPKLLIYAASLSQSGVPSRF 61
 4 LTQSPSSLSASVGDRTVITCRASQDISRYLNMWYQKPKAPKLLIYAASLSQSGVPSRF 63
 Db 62 GSGYGTDFTLTITSSLOPEDFASVYCOESLSASTFGCGTKVEIKR 105
 64 GSGSGTDFLTITSSLOPEDFATVYCOQSYSTPPTFGCGTKVEIKR 107

RESULT 14

S31977

Ig kappa chain - human
 C:Species: Homo sapiens (man)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
 C:Accession: S31977
 R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992
 A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
 A:Reference number: S31977
 A:Accession: S31977
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-108 <POR>
 A:Cross-references: EMBL:Z15073
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.5%; Score 437; DB 2; Length 108;
 Best Local Similarity 82.9%; Pred. No. 1.1e-33;
 Matches 87; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITCRASQDISRYLNMWYQKPKAPKLLIYAASLSQSGVPSRF 61
 4 MTQSPSSLSASVGDRTVITCRASQDISRYLNMWYQKPKAPKLLIYAASLSQSGVPSRF 63
 Db 62 GSGYGTDFTLTITSSLOPEDFASVYCOESLSASTFGCGTKVEIKR 106
 64 GSGSGTDFLTITSSLOPEDFATVYCOQSYSTPPTFGCGTKVEIKR 108

RESULT 15

S31983
 Ig kappa chain - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S31983
 R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992
 A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
 A:Reference number: S31977
 A:Accession: S31983
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-109 <POR>
 A:Cross-references: EMBL:Z15073; NID:G38497; PIDN:CAA78788.1; PID:G38498
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 436; DB 2; Length 109;
 Best Local Similarity 79.0%; Pred. No. 1.3e-33;
 Matches 83; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITCRASQDISRYLNMWYQKPKAPKLLIYAASLSQSGVPSRF 61
 4 MTQSPSSLSASVGDRTVITCRASQDISRYLNMWYQKPKAPKLLIYAASLSQSGVPSRF 63
 Db 62 GSGYGTDFTLTITSSLOPEDFASVYCOESLSASTFGCGTKVEIKR 106
 64 GSGSGTDFLTITSSLOPEDFATVYCOQSYSTPPTFGCGTKVEIKR 108

Search completed: February 10, 2004, 18:41:10
 Job time: 11.9212 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 17:48:48 ; Search time 5.94242 Seconds
(without alignments)
838.855 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543
Sequence: 1 ELTGSPSSLSASVGDRTVIS.....QESLSASTPQGTKEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	436	80.3	129	1 KVIW_HUMAN	P04431 homo sapien
2	433	79.7	108	1 KVIK_HUMAN	P01597 homo sapien
3	430	79.2	108	1 KVIH_HUMAN	P01600 homo sapien
4	420	77.3	108	1 KVIH_HUMAN	P01606 homo sapien
5	416	76.6	108	1 KVIK_HUMAN	P01598 homo sapien
6	414	76.2	108	1 KVIK_HUMAN	P01603 homo sapien
7	413	76.1	108	1 KVIK_HUMAN	P04430 homo sapien
8	412	75.9	108	1 KVIK_HUMAN	P01607 homo sapien
9	409	75.3	108	1 KVIK_HUMAN	P01599 homo sapien
10	408	75.1	108	1 KVIK_HUMAN	P01605 homo sapien
11	407	75.0	108	1 KVIK_HUMAN	P01594 homo sapien
12	406	74.8	108	1 KVIK_HUMAN	P01610 homo sapien
13	404	74.4	108	1 KVIK_HUMAN	P01593 homo sapien
14	399.5	73.6	107	1 KVIK_HUMAN	P01596 homo sapien
15	399	73.5	108	1 KVIK_HUMAN	P01611 homo sapien
16	398	73.3	108	1 KVIK_HUMAN	P01608 homo sapien
17	397	73.1	129	1 KVIK_HUMAN	P01604 homo sapien
18	397	72.9	108	1 KVIK_HUMAN	P04432 homo sapien
19	396	72.9	108	1 KVIK_HUMAN	P01609 homo sapien
20	391	72.0	108	1 KVIK_HUMAN	P01612 homo sapien
21	385.5	71.0	109	1 KVIK_HUMAN	P01595 homo sapien
22	384	70.7	108	1 KVIK_HUMAN	P01653 mus musculu
23	376	69.2	108	1 KVIK_HUMAN	P01653 mus musculu
24	373	68.7	108	1 KVIK_HUMAN	P01653 mus musculu
25	370.5	68.2	109	1 KVIK_HUMAN	P01650 mus musculu
26	370	68.1	108	1 KVIK_HUMAN	P01620 mus musculu
27	368.5	67.9	109	1 KVIK_HUMAN	P01622 homo sapien
28	368.5	67.9	109	1 KVIK_HUMAN	P01622 homo sapien
29	368	67.8	108	1 KVIK_HUMAN	P01647 mus musculu
30	368	67.8	108	1 KVIK_HUMAN	P01648 mus musculu
31	368	67.8	117	1 KVIK_HUMAN	P01648 mus musculu
32	367.5	67.7	129	1 KVIK_HUMAN	P18136 homo sapien
33	366.5	67.5	129	1 KVIK_HUMAN	P18135 homo sapien

34	366	67.4	114	1 KVIK_HUMAN	P01625 homo sapien
35	366	67.4	117	1 KVIK_HUMAN	P01601 homo sapien
36	365	67.2	108	1 KVIK_HUMAN	P01644 mus musculu
37	365	67.2	108	1 KVIK_HUMAN	P01646 mus musculu
38	365	67.2	134	1 KVIK_HUMAN	P06314 homo sapien
39	364	67.0	108	1 KVIK_HUMAN	P01651 mus musculu
40	363	66.9	111	1 KVIK_HUMAN	P01665 mus musculu
41	362	66.7	111	1 KVIK_HUMAN	P01664 mus musculu
42	361	66.5	108	1 KVIK_HUMAN	P01645 mus musculu
43	360	66.3	108	1 KVIK_HUMAN	P01645 mus musculu
44	358	65.9	111	1 KVIK_HUMAN	P01667 mus musculu
45	357	65.7	128	1 KVIK_HUMAN	P01637 mus musculu

ALIGNMENTS

RESULT 1	ID	KVIW_HUMAN	STANDARD	PRT	129 AA.
AC	P04431				
DT	13-AUG-1987	(Rel. 05, Created)			
DT	13-AUG-1987	(Rel. 05, Last sequence update)			
DT	15-JUL-1999	(Rel. 38, Last annotation update)			
DE	Ig kappa chain V-I region Walker precursor.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo;				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=85014148; PubMed=6091049;				
RA	Klobeck H.G., Combrato G., Zachau H.G.;				
RT	"Immunoglobulin genes of the kappa light chain type from two human				
RT	lymphoid cell lines are closely related."				
RL	Nucleic Acids Res. 12:6995-7006(1984).				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL; X00965; CAA25477.1; ALT_TERM.				
DR	PIR; A01883; K1HUKM.				
DR	HSSP; P01607; IREI.				
DR	GO; GO:0005576; C:extracellular; NAS.				
DR	GO; GO:0003823; F:antigen binding activity; NAS.				
DR	GO; GO:0006955; P:immune response; NAS.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003006; Ig-MHC.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; IGV_1.				
DR	PROSITE; PS50835; IG_LIKE_1.				
KW	Immunoglobulin V region, Signal.				
FT	SIGNAL	1	22		IG KAPPA CHAIN V-I REGION WALKER.
FT	CHAIN	23	129		FRAMEWORK-1.
FT	DOMAIN	23	45		COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	46	56		FRAMEWORK-2.
FT	DOMAIN	57	71		COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	72	78		FRAMEWORK-3.
FT	DOMAIN	79	110		COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN	111	119		FRAMEWORK-4.
FT	DOMAIN	120	129		BY SIMILARITY.
FT	DISULFID	45	110		
FT	NON_TER	129	129		
SQ	SEQUENCE	129 AA;	14069 MW;		F941PA07D4AFC2P9 CRC64;
Query Match		80.3%;	Score 436;	DB 1;	Length 129;
Best Local Similarity		81.9%;	Pred. No. 6.1e-40;		

Matches 86; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVITISCRASQRIINTYLNMYOHKPKAPKLLIYAASSLQSGVPSRF 60
 DB 25 QMTQSPSSLSASVGDVITITCRASQSIINTYLNMYOHKPKAPKLLIYAASSLQSGVPSRF 84
 QY 61 SSGSGYTDFTLTITSSIQPEDFASVYCOESLSASVYTCGQGTVEIKR 105
 DB 65 SSGSGYTDFTLTITSSIQPEDSATYVYCOQSYTITTCGQGTVEIKR 129

RESULT 2

KVLE HUMAN
 ID KVLE HUMAN STANDARD; PRT; 108 AA.

AC P01567;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region DEE.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1)
 RP SEQUENCE.
 RX MEDLINE=72053133; PubMed=5124396;
 RA Milstein C.P., Deveron E.V.,
 RT "The amino acid sequence of a human kappa light chain.",
 RL Biochem. J. 123:945-958(1971).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR PIR; A01865; KIHUDE.
 DR HSSP; P01607; IREI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11661 MW; BDDEE350017PIE51 CRC64;

Query Match 79.7%; Score 433; DB 1; Length 108;
 Best Local Similarity 77.4%; Pred. No. 1e-39;

Matches 82; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVITISCRASQRIINTYLNMYOHKPKAPKLLIYAASSLQSGVPSRF 60
 DB 3 ZMTQSPSSLSASVGDVITITCRASQSIINTYLNMYOHKPKAPKLLIYAASSLQSGVPSRF 62
 QY 61 SSGSGYTDFTLTITSSIQPEDFASVYCOESLSASVYTCGQGTVEIKR 106
 DB 63 SSGSGYTDFTLTITSSIQPEDFATYVYCOQSYTITTCGQGTVEIKR 108

RESULT 3

KVH HUMAN
 ID KVH HUMAN STANDARD; PRT; 108 AA.

AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region Hau.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1)
 RP SEQUENCE.
 RX MEDLINE=71032830; PubMed=4097974;
 RA Watanabe S., Hlischmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 chain of subgroup I (Bence-Jones Protein Hau) : subdivision within
 subgroups.",
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
 DR PIR; A01868; KIHUHU.
 DR HSSP; P80362; IWTU.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones Protein.

FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 79.2%; Score 430; DB 1; Length 108;
 Best Local Similarity 78.3%; Pred. No. 2.2e-39;
 Matches 83; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVITISCRASQRIINTYLNMYOHKPKAPKLLIYAASSLQSGVPSRF 60
 DB 3 QMTQSPSSLSASVGDVITITCRASQSIINTYLNMYOHKPKAPKLLIYAASSLQSGVPSRF 62
 QY 61 SSGSGYTDFTLTITSSIQPEDFASVYCOESLSASVYTCGQGTVEIKR 106
 DB 63 SSGSGYTDFTLTITSSIQPEDFATYVYCOQSYTITTCGQGTVEIKR 108

RESULT 4

KVIN HUMAN
 ID KVIN HUMAN STANDARD; PRT; 108 AA.

AC P01606;
 DT 21-JUL-1986 (Rel. 01, Created).
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region OU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1)
 RP SEQUENCE.
 RX MEDLINE=70201507; PubMed=5447531;
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
 RT "Macroglobulin structure: variable sequence of light and heavy
 chains.",
 RL Science 169:56-59(1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 MACROGLOBULIN.

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DR PIR; A01872; KIHUOU.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283DA424105827E CRC64;

Query Match 77.3%; Score 420; DB 1; Length 108;
Best Local Similarity 68.9%; Pred. No. 2.6e-38;
Matches 73; Conservative 22; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGDRTYISCRASQRIINTYIMYQHKRGKAPKLLIYAASSLSQGVPSRF 60
DB 3 QMTSPSTLSASVGDRTYITCRASZTISSTYLMWYZZKRGKAPBLIIYAASBLHSGVPSRF 62
QY 61 SSGSGTDFTLTISLQFEDPASYCYQESLSASYTFGGGTVEIK 106
DB 63 SSGSGTDFTLTISLQFEDPASYCYQESLSASYTFGGGTVEIK 108

RESULT 5
KV1F HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D.; Cunningham B.A.; Rutishauser U.; Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RL Biochemistry 9:3155-3161(1970).
RT "Biochemistry 9:3188-3196(1970).
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT "Biochemistry 9:3188-3196(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD234F2F4D88823 CRC64;

Query Match 76.6%; Score 416; DB 1; Length 108;
Best Local Similarity 77.1%; Pred. No. 7e-38;
Matches 81; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGDRTYISCRASQRIINTYIMYQHKRGKAPKLLIYAASSLSQGVPSRF 60
DB 3 QMTSPSTLSASVGDRTYITCRASQRIINTYIMYQHKRGKAPKLLIYAASSLSQGVPSRF 62
QY 61 SSGSGTDFTLTISLQFEDPASYCYQESLSASYTFGGGTVEIK 105
DB 63 SSGSGTDFTLTISLQFEDPASYCYQESLSASYTFGGGTVEIK 107

RESULT 6
KV1K HUMAN STANDARD; PRT; 108 AA.
AC P01603;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Ka.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76189985; PubMed=818073;
RA Shinoda T.;
RT "Comparative structural studies on the light chains of human
RT immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL J. Biochem. 77:1277-1286(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR HSSP; P80362; IWTU.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11900 MW; 768839FBE52F4B CRC64;

Query Match 76.2%; Score 414; DB 1; Length 108;
Best Local Similarity 70.8%; Pred. No. 1.2e-37;

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Qy	Db	Qy	Db
1	3	61	63
ELTSPSSLSASVDR	QMTQSPSSLSASVDR	SGSSTGYDFTLTIS	SGSSGSGDYFTLTIS
YTIICRA	YTIICQA	SLQPED	SLQPED
NTNLT	QDIK	YCOES	YCOQY
YOHNG	QIKN	SLAST	SLAST
PGAPK	PGAPK	TCQCK	TCQCK
PLTL	PLTL	IKR	IKR
LYAASS	LYAASS		
SLQSVSR	SLQSVSR		
60	62		

RESULT 9

KG	KGID	HUMAN	STANDARD	PRT	108 AA
AC	P01539				
DT	21-JUL-1986	(Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, Last sequence update)			
DT	15-JUN-1999	(Rel. 38, Last annotation update)			
DE	IG kappa chain V-I region Gal.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				

RESULT	10
KVIM	HUMAN
ID_KVIM	HUMAN
AC	P01605;
DT	21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE IG kappa chain V-I region 1ay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;

	RESULT	11
KY1B	HUMAN	
ID	KY1B_HUMAN	STANDARD; PRT; 108 AA.
AC	P01594;	
DI	21-JUL-1986 (Rel. 01, Created)	
DT	21-JUL-1986 (Rel. 01, Last sequence update)	
DT	15-SEP-2003 (Rel. 42, Last annotation update)	
DE	IG kappa chain V-I region AU.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE.	
RX	MEDLINE=72189444; Pubmed=5028201;	
RA	Scheel H., Hilschmann N.,	
RT	"Rule of antibody structure. The primary structure of a monoclonal	

RT Immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 RT protein Au.);
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehlfammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the
 Bence-Jones protein Au.";
 RL Biophys. Struct. Mech. 1:139-146(1975).
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
 CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
 CC REGION OF THE KAPPA CHAIN REI.
 CC -1- MISCELLANEOUS: THIS C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
 CC PIR; A91653; KIHUV.
 DR PDB; 1JVS; 30-JAN-02.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 FRAMEWORK-4.
 FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11939 MW; E801187E6F6FB9 CRC64;
 Query Match 75.8%; Score 407; DB 1; Length 108;
 Best Local Similarity 75.5%; Pred. No. 6.5e-37;
 Matches 80; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
 QY 1 ELTQSPSSISASVGDRTVITSCRASORINTYLNWYQHKPGKAPKLLIYAASLSQGVPSRF 60
 DB 3 QMTQSSSSISASVGDRTVITSCRASODISDLYNYYQKPGKAPKLLIYDSSNLSGVPSRF 62
 QY 61 SSGSGYDTFTLTITSSLOFEDFASVYCOESLSASVYFGQGTKEIKR 106
 DB 63 SSGSGSAHFTTITSSLOPEDIAITYYCOQYDYLPTFGQGTKEIKR 108
 RESULT 12
 KXIR HUMAN STANDARD; PRT; 108 AA.
 ID KXIR HUMAN
 AC P01610;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 19 kappa chain V-I region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83273707; PubMed=6410398;
 RA Goni F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM
 RT (protein WEA) with antibody activity against 3,4-pyruvylated
 RT galactose in Klebsiella polysaccharides K30 and K33.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY

CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 CC WALDENSTROM'S MACROGLOBULINEMIA.
 CC PIR; A01876; KIHUWE.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Monoclonal antibody.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 FRAMEWORK-4.
 FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;
 Query Match 74.8%; Score 406; DB 1; Length 108;
 Best Local Similarity 75.5%; Pred. No. 8.3e-37;
 Matches 80; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
 QY 1 ELTQSPSSISASVGDRTVITSCRASORINTYLNWYQHKPGKAPKLLIYAASLSQGVPSRF 60
 DB 3 QMTQSSSSISASVGDRTVITSCRASQIRNDLTWYQKPGTAPKRLIYGATSSLSQGVPSRF 62
 QY 61 SSGSGYDTFTLTITSSLOFEDFASVYCOESLSASVYFGQGTKEIKR 106
 DB 63 SSGSGTEFTLTITSSLOPEDFATYCYCLOYSPPWTFGQGTKEIKR 108
 RESULT 13
 KXIA HUMAN STANDARD; PRT; 108 AA.
 ID KXIA HUMAN
 AC P01593;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 19 kappa chain V-I region AG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=69234734; PubMed=4893682;
 RA Titani K., Shinoda T., Putnam F.W.;
 RT "The amino acid sequence and the location of the disulfide bridges.";
 RT complete sequence and the location of the disulfide bridges.";
 RL J. Biol. Chem. 244:3550-3560(1969).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
 CC PIR; A01861; KIHUAG.
 DR HSSP; P01607; 1REI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 74.4%; Score 404; DB 1; Length 108;
 Best Local Similarity 73.6%; Pred. No. 1.4e-36;
 Matches 78; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVITSCRASORINTYLNWYOHKPKAKPLLIYAASSLSQGVPSRF 60
 DB 3 QMTOSPSLSASVGRVITTCASQDINHLYMWYQOGPKKAKPLIYDASNLGVPSRF 62
 QY 61 SSGSGTDFTLTISLQFEDFASYYCOESLSASTYFGGCTVKEIR 106
 DB 63 SSGSGTDFTLTISLQFEDFATYFCQYDTLPRTFGGCTVKEIR 108

RESULT 14
 ID KVID HUMAN STANDARD; PRT; 107 AA.
 AC P01596;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region CAR.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75075135; PubMed=4216454;
 RA Milstein C.P.; Deverson E.V.;
 RT "Primary structure of kappa light chain from a human myeloma protein."
 RT Eur. J. Biochem. 49:377-391(1974).
 CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A01864; KIHUAR.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Glycoprotein.
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
 FT NON TER 107 107
 SQ SEQUENCE 107 AA; 11703 MW; E1BFD0F9844C3346 CRC64;

Query Match 73.6%; Score 399.5; DB 1; Length 107;
 Best Local Similarity 71.7%; Pred. No. 4.1e-36;
 Matches 76; Conservative 18; Mismatches 11; Indels 1; Gaps 1;

QY 1 ELTOSPSLSASVGRVITSCRASORINTYLNWYOHKPKAKPLLIYAASSLSQGVPSRF 60
 DB 3 QMTOSPSLSASVGRVITTCASQDINHLYMWYQOGPKKAKPLIYDASNLGVPSRF 62
 QY 61 SSGSGTDFTLTISLQFEDFASYYCOESLSASTYFGGCTVKEIR 106
 DB 63 SSGSGTDFTLTISLQFEDFATYFCQYDTLPRTFGGCTVKEIR 108

RESULT 15
 ID KVID HUMAN STANDARD; PRT; 108 AA.
 AC P01611;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Wes.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81092279; PubMed=6778806;
 RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
 RT "Preparative separation of the tryptic hydrolyzate of a protein by high-pressure liquid chromatography. The primary structure of a monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein Wes)."
 RT Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
 CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01877; KIHUMS.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 24 34 FRAMEWORK-1.
 FT DOMAIN 24 35 49 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 50 56 FRAMEWORK-2.
 FT DOMAIN 50 57 88 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 89 97 FRAMEWORK-3.
 FT DOMAIN 89 98 107 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 88 FRAMEWORK-4.
 FT NON TER 108 108 BY SIMILARITY.
 SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60B45 CRC64;

Query Match 73.5%; Score 399; DB 1; Length 108;
 Best Local Similarity 73.6%; Pred. No. 4.7e-36;
 Matches 78; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVITSCRASORINTYLNWYOHKPKAKPLLIYAASSLSQGVPSRF 60
 DB 3 QMTOSPSLSASVGRVITTCASQDINHLYMWYQOGPKKAKPLIYDASNLGVPSRF 62
 QY 61 SSGSGTDFTLTISLQFEDFASYYCOESLSASTYFGGCTVKEIR 106
 DB 63 SSGSGTDFTLTISLQFEDFATYFCQYDTLPRTFGGCTVKEIR 108

Search completed: February 10, 2004, 18:36:31
 Job time : 6.94242 secs

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DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 80.9%; Score 439.5; DB 4; Length 107;
Best Local Similarity 82.1%; Pred. No. 5.9e-41;
Matches 87; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 ELTSPSSLSASVGDRTVISCRAQRINTYLMYQHKPKGAPKLLIYAASSLSQGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITICRASQSIISNTLMYQKPKGAPKLLIYAASSLSQGVPSRF 62
QY 61 GSGSYGDTFTLTISLQPEDFPASYYCCESLSASTFGCGTVEIKR 106
DB 63 GSGSGYDTFTLTISGLQAEDEFATYYCQSYSA-LTFGPGTKVDIR 107

RESULT 4
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive Immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 77.7%; Score 422; DB 4; Length 108;
Best Local Similarity 80.0%; Pred. No. 5.2e-39;
Matches 84; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVISCRAQRINTYLMYQHKPKGAPKLLIYAASSLSQGVPSRF 61
DB 4 MTQSPSSLSASTGDRVITICRMSGISISYLAWYQKPKGAPKLLIYAASSLSQGVPSRF 63
QY 62 GSGYGTDTFTLTISLQPEDFPASYYCQSSLSASTFGCGTVEIKR 106
DB 64 GSGSGYDTFTLTISCLQSEDEFATYYCQSYSPFPFGGTVEIKR 108

RESULT 5
Q9UL70

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ID 09UL70      PRELIMINARY;      PRT;      108 AA.
AC 09UL70:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
   Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER      1      1
FT NON_TER      108    108
SQ SEQUENCE      108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

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Query Match      77.3%; Score 420; DB 4; Length 108;
Best Local Similarity 79.2%; Pred. No. 8.6e-39;
Matches 84; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ELTOSPSLSASVGRVTISCRASORINTYLMWYOHKKGAKPKLIYAASSLSQGVPSRF 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSLSASVGRVTITCRASGIGISNYLAWYQKRGKPKLIYAASSLSQGVPSRF 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 SGGSGYTDFTLTISLQFEDFASYYCOESLSASYTFGQGTVEIKR 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SGGSGYTDFTLTISLQFEDFATYYCOYHNLPTFGGTVDPR 108
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RESULT 6
Q9UL83      PRELIMINARY;      PRT;      108 AA.
ID 09UL83:
AC 09UL83:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
   Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P80362; IMTL.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

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FT NON_TER      1      1
FT NON_TER      108    108
SQ SEQUENCE      108 AA; 11834 MW; 9F9C5A92BBA6EEA CRC64;

Qy 2 LTQSPSSLSASVGRVTISCRASORINTYLMWYOHKKGAKPKLIYAASSLSQGVPSRF 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 MTQSPATLSVSPGERATLSCASQSVSSNLAWYQKRGKPKLIYAASSLSQGVPSRF 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 62 SGGSGYTDFTLTISLQFEDFASYYCOESLSASYTFGQGTVEIKR 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 SGGSGYTDFTLTISLQFEDFATYYCOYHNLPTFGGTVDPR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 7
Q96PF6      PRELIMINARY;      PRT;      116 AA.
ID 096PF6:
AC 096PF6:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Kappa 1 light chain variable region (Fragment).
CN SDKL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
   contributions of Ig V(L) germ line gene use and clonal plasma cell
   burden."
RL Blood 98:714-720(2001).
DR EMBL; AF361758; AAKS1465.1;
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER      1      1
FT NON_TER      116    116
SQ SEQUENCE      116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

```

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Query Match      68.3%; Score 371; DB 4; Length 116;
Best Local Similarity 67.9%; Pred. No. 2.5e-33;
Matches 72; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

```

```

Qy 1 ELTQSPSSLSASVGRVTISCRASORINTYLMWYOHKKGAKPKLIYAASSLSQGVPSRF 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSLSASVGRVTITCRASGIGISNYLAWYQKRGKPKLIYAASSLSQGVPSRF 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 SGGSGYTDFTLTISLQFEDFASYYCOESLSASYTFGQGTVEIKR 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SGGSGATNFTVTITSLQFEDFATYYCOYHNLPTFGGTVDPR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 8
Q9OYF0      PRELIMINARY;      PRT;      298 AA.
ID 09OYF0:
AC 09OYF0:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE CN 8 scFv.
CN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=20183911; PubMed=10706611;
RA Shiohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
recognizing a cell polarity by using a phage display subtraction
method."
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590 (2000).
DR EMBL; AB036341; BAA88633.1; -
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; 50F96B8A17004317 CRC64;

Query Match 67.4%; Score 366; DB 11; Length 238;
Best Local Similarity 67.0%; Pred. No. 2.9e-32;
Matches 71; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

QY 1 ELTGSSSSLSASVGDVVTISCRASQRIINTYLMWQHKGKAPKLLIYAASSLSQGVPSRF 60
DB 175 ELTGSSSSLSASVGEVVTITCRASGNINHWYQKQKQSPLLIYNKKTADGVPSRF 234
61 SSGSGVDTFTLTITSSLOFEDFASYYCOESLSASVTFGQGTKEIKR 106
DB 235 SSGSGSTGYSLKINSLOPEDFGSYCOHFWTTPTTGGGTKEIKR 280

RESULT 9
O9R1A5 PRELIMINARY; PRT; 214 AA.
AC O9R1A5;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (scFv)."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -
DR HSSP; P01679; 2F8J.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE9395E2A CRC64;

Query Match 67.0%; Score 364; DB 11; Length 214;
Best Local Similarity 64.2%; Pred. No. 3.2e-32;
Matches 68; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

QY 1 ELTGSSSSLSASVGDVVTISCRASQRIINTYLMWQHKGKAPKLLIYAASSLSQGVPSRF 60
DB 3 QLTGSSSSSWASVAGVVTITCKASQDINSYLSWFOQKPKGSPKTLIYRANRLVDGVPSRF 62

QY 61 SSGSGVDTFTLTITSSLOFEDFASYYCOESLSASVTFGQGTKEIKR 106
DB 63 SSGSGGDYSLTISLEEDMKGIYCLQDEPFPTFGGTKEIKR 108

RESULT 10
O9IWF8 PRELIMINARY; PRT; 234 AA.
AC O9IWF8;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Query Match 66.5%; Score 361; DB 11; Length 234;
Best Local Similarity 65.1%; Pred. No. 7.6e-32;
Matches 69; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

QY 1 ELTGSSSSLSASVGDVVTISCRASQRIINTYLMWQHKGKAPKLLIYAASSLSQGVPSRF 60
DB 23 QMTQTSSLSASLIGRVITISCRASQDISNHWYQKQKGVKLLIYTSRLYLGVPSRF 82
61 SSGSGVDTFTLTITSSLOFEDFASYYCOESLSASVTFGQGTKEIKR 106
DB 83 SSGSGSTGYSLTISNLEQEDIAFYCOQGNTPPTFGGTKEIKR 128

RESULT 11
O9R062 PRELIMINARY; PRT; 234 AA.
AC O9R062;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027418; AAH27418.1; -
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.

SO SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;
Query Match 66.5%; Score 351; DB 11; Length 234;
Best Local Similarity 67.0%; Pred. No. 7,6e-32;
Matches 71; Conservative 13; Mismatches 22; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLSQSGVPSRF 60
DB 23 QMTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLSQSGVPSRF 82
QY 61 SSGSGVGTFTLTISLSQFEDFPASYCOESLSASYTFPGGTVEIKR 106
DB 83 SSGSGGTHTSLTISLNPEDIPATYTCQYQSGPFTFGGTLEIKR 128
RESULT 12
Q8NEK1 PRELIMINARY; PRT; 234 AA.
Q8NEK1
AC Q8NEK1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC030813; AAA30813.1; -.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_2.
DR SMART; SM00407; IGV_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25530 MW; 6316B8DEF8D132F8 CRC64;
Query Match 66.3%; Score 360; DB 4; Length 234;
Best Local Similarity 64.8%; Pred. No. 9,8e-32;
Matches 68; Conservative 17; Mismatches 20; Indels 0; Gaps 0;
QY 2 LTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLSQSGVPSRF 61
DB 24 MTQSPATLSVSPGEKATISCRASQSVSTNLAWYQOTPOSPLVLYGASSSRASGVPSRF 83
QY 62 GSGVGTFTLTISLSQFEDFPASYCOESLSASYTFPGGTVEIKR 106
DB 84 GSGGTFTLTISLSQFEDFPASYTCQYQNKMPHTFGGTLEIKR 128
RESULT 13
Q920E6 PRELIMINARY; PRT; 109 AA.
Q920E6
AC Q920E6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307938; AAL09422.1; -.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11943 MW; DAD3F98B5DD1501 CRC64;
Query Match 66.1%; Score 359; DB 11; Length 109;
Best Local Similarity 65.1%; Pred. No. 4,9e-32;
Matches 69; Conservative 15; Mismatches 22; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLSQSGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLSQSGVPSRF 62
QY 61 SSGSGVGTFTLTISLSQFEDFPASYCOESLSASYTFPGGTVEIKR 106
DB 63 SSGSGGTHTSLTISLNPEDIPATYTCQYQSGPFTFGGTLEIKR 108
RESULT 14
Q920E9 PRELIMINARY; PRT; 111 AA.
Q920E9
AC Q920E9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307935; AAL09419.1; -.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00407; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 12046 MW; 1E46988AA6858526 CRC64;
Query Match 66.1%; Score 359; DB 11; Length 111;
Best Local Similarity 63.9%; Pred. No. 5e-32;
Matches 69; Conservative 16; Mismatches 19; Indels 4; Gaps 1;
QY 2 LTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLSQSGVPSRF 57
DB 4 LTQSPASSLSASVGDRTVITSCRASQSVSTNLAWYQOTPOSPLVLYGASSSRASGVPSRF 63
QY 58 SRFSGVGTFTLTISLSQFEDFPASYCOESLSASYTFPGGTVEIKR 105
DB 64 ARFSGSGVGTFTLTINHPVEEDIPATYTCQYQNRRLPTFGGTLEIKR 111
RESULT 15
Q91WS9

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ID 091WS9          PRELIMINARY;      PRT: 233 AA.
AC 091WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PR00047; IG_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 65.7%; Score 357; DB 11; Length 233;
Best Local Similarity 67.0%; Pred. No. 2.1e-31;
Matches 71; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASGVDRVTISCRASORINTYLNWYOHKPGKAPKLLIYAASLSQGVPSRF 60
DB 22 QMTQTSSLSASLGDRVTISCSGSGGIANYLNWYQQKPDGTVKLLIYTTSLHSGVPSRF 81

QY 61 SSGSGYGTDFLTLLTISLQFEDFASVYCOESLSASVTFGGTKVEIKR 106
DB 82 SSGSGSGTDYSLTISNLEPEDIAITYCOQRYRLPMTFGGTKEIKR 127

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Search completed: February 10, 2004, 18:39:22
 Job time : 26.0545 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:32:44 ; Search time 10.9212 Seconds

(without alignments)
410.664 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543
Sequence: 1 ELVQSPSSLSASVGDRTYIS.....QESLSASTFGQTKVRIK 106Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCrUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1est.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	475	87.5	107	1	US-08-276-852-104 Sequence 104, App
2	475	87.5	107	1	US-08-899-575-104 Sequence 104, App
3	475	87.5	107	1	US-08-899-575-104 Sequence 104, App
4	475	87.5	107	5	PCT-US95-08743-104 Sequence 104, App
5	474	87.3	107	3	US-09-240-274-179 Sequence 179, App
6	472	86.9	107	3	US-09-240-274-175 Sequence 33, App1
7	472	86.9	107	3	US-09-240-274-176 Sequence 175, App
8	472	86.9	107	3	US-09-240-274-176 Sequence 176, App
9	471	86.7	107	3	US-09-240-274-156 Sequence 156, App
10	468	86.2	107	3	US-09-240-274-36 Sequence 36, App1
11	467	86.0	107	1	US-08-276-852-105 Sequence 105, App
12	467	86.0	107	1	US-08-899-575-105 Sequence 105, App
13	467	86.0	107	1	US-08-899-575-105 Sequence 105, App
14	467	86.0	107	5	PCT-US95-08743-105 Sequence 105, App
15	464.5	85.5	108	3	US-09-240-274-32 Sequence 32, App1
16	464.5	85.5	108	3	US-09-240-274-43 Sequence 43, App1
17	464	85.5	107	3	US-09-240-274-37 Sequence 37, App1
18	462	85.1	107	3	US-09-240-274-38 Sequence 38, App1
19	462	85.1	107	3	US-09-240-274-39 Sequence 39, App1
20	461	84.9	107	3	US-09-240-274-158 Sequence 158, App
21	460.5	84.8	108	3	US-09-240-274-167 Sequence 167, App
22	459.5	84.6	108	3	US-09-240-274-163 Sequence 163, App
23	458	84.3	107	3	US-09-240-274-35 Sequence 35, App1
24	458	84.3	107	3	US-09-240-274-173 Sequence 173, App
25	457	84.2	104	1	US-08-379-057-29 Sequence 29, App1
26	457	84.2	104	1	US-08-276-852-106 Sequence 106, App
27	457	84.2	104	1	US-08-899-575-106 Sequence 106, App

28	457	84.2	104	1	US-08-899-575-106 Sequence 106, App
29	457	84.2	104	5	PCT-US95-08743-106 Sequence 106, App
30	457	84.2	107	3	US-09-240-274-40 Sequence 40, App1
31	456	84.0	107	3	US-09-240-274-44 Sequence 44, App1
32	452	83.2	107	3	US-09-240-274-172 Sequence 172, App
33	452	83.2	107	3	US-09-240-274-174 Sequence 174, App
34	451.5	83.1	108	1	US-08-276-852-109 Sequence 109, App
35	451.5	83.1	108	1	US-08-899-575-109 Sequence 109, App
36	451.5	83.1	108	1	US-08-899-575-109 Sequence 109, App
37	451.5	83.1	108	3	US-09-240-274-41 Sequence 41, App1
38	451.5	83.1	108	5	PCT-US95-08743-109 Sequence 109, App
39	451	83.1	107	3	US-09-240-274-168 Sequence 168, App
40	451	83.1	108	4	US-09-025-7698-14 Sequence 14, App1
41	451	83.1	109	2	US-07-934-373C-3 Sequence 3, App1
42	451	83.1	109	3	US-08-437-642B-3 Sequence 3, App1
43	451	83.1	109	4	US-08-146-206C-3 Sequence 3, App1
44	451	83.1	109	5	PCT-US93-07832-3 Sequence 3, App1
45	450	82.9	107	3	US-09-240-274-34 Sequence 34, App1

ALIGNMENTS

RESULT 1
US-08-276-852-104
Sequence 104, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Bardas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-104

Query Match 87.5%; Score 475; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 7e-39;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITISCRASQRIINLYLMWYQHKPKAPKLLIYAASSLSQGVPSRF 60
DB 1 ELTQSPSSLSASVGRVITITCRASQSISSYLMWYQOKPKAPKLLIYAASSLSQGVPSRF 60

QY 61 SSGSGTDTFTLTISLQFEDFASYYQESLSASYYTGQGTKEIKR 106
DB 61 SSGSGTDTFTLTISLQPEDFATYYCQGSYSTPYTFGQGTKEIKR 106

RESULT 2
US-08-899-575-104
; Sequence 104, Application US/08899575

; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Letner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSER: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match 87.5%; Score 475; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 7e-39;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITISCRASQRIINLYLMWYQHKPKAPKLLIYAASSLSQGVPSRF 60
DB 1 ELTQSPSSLSASVGRVITITCRASQSISSYLMWYQOKPKAPKLLIYAASSLSQGVPSRF 60

QY 61 SSGSGTDTFTLTISLQFEDFASYYQESLSASYYTGQGTKEIKR 106
DB 61 SSGSGTDTFTLTISLQPEDFATYYCQGSYSTPYTFGQGTKEIKR 106

RESULT 3
US-08-899-575-104
; Sequence 104, Application US/08899575

; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Letner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSER: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match 87.5%; Score 475; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 7e-39;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITISCRASQRIINLYLMWYQHKPKAPKLLIYAASSLSQGVPSRF 60
DB 1 ELTQSPSSLSASVGRVITITCRASQSISSYLMWYQOKPKAPKLLIYAASSLSQGVPSRF 60

QY 61 SSGSGTDTFTLTISLQFEDFASYYQESLSASYYTGQGTKEIKR 106
DB 61 SSGSGTDTFTLTISLQPEDFATYYCQGSYSTPYTFGQGTKEIKR 106

RESULT 4
PCT-US95-08743-104
; Sequence 104, Application PC/TUS9508743


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; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-104

Query Match      87.5%; Score 475; DB 5; Length 107;
Best Local Similarity 87.7%; Pred. No. 7e-39;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Cy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITCRASQSISSYINWYQOKRGKAPKLLIYAASSLSQGVPSRF 60

Cy 61 SGGSGTDFTLTISLQFEDPASYCCOBSLSASTFFGGTVEIKR 106
Db 61 SGGSGTDFTLTISLQPEDPATYCCOQSYSTPFFGGTVEIKR 106

RESULT 5
US-09-240-274-179
; Sequence 179, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-179

Query Match      87.3%; Score 474; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 8.7e-39;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Cy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQSIGIYNWYQOKRGKAPKLLIYAASSLSQGVPSRF 61

Cy 61 SGGSGTDFTLTISLQFEDPASYCCOBSLSASTFFGGTVEIKR 106
Db 62 SGGSGTDFTLTISLQPEDPATYCCOQSYSTPFFGGTVEIKR 107
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RESULT 6
US-09-240-274-33
; Sequence 33, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-240-274-33

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.4e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Cy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQSISSYINWYQOKRGKAPKLLIYAASSLSQGVPSRF 61

Cy 61 SGGSGTDFTLTISLQFEDPASYCCOBSLSASTFFGGTVEIKR 106
Db 62 SGGSGTDFTLTISLQPEDPATYCCOQSYSTLMTFFGGTVEIKR 107

RESULT 7
US-09-240-274-175
; Sequence 175, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-175

Query Match      86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.4e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Cy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRASQSISSYINWYQOKRGKAPKLLIYAASSLSQGVPSRF 61
```


FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-105

Query Match 86.0%; Score 467; DB 1; Length 107;
Best Local Similarity 86.8%; Pred. No. 4.1e-38;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSLASVGDRTVITSCRASQRIINTYLNWYQHKRGA PKLLIYAASSLSQGVPSRF 60
Db 1 ELTQSPSLASVGDRTVITSCRASQRIINTYLNWYQHKRGA PKLLIYAASSLSQGVPSRF 60

Qy 61 SGSGVGTDFLTITISLQFEDFASYYCOESLSASTYFGGTVEIKR 106
Db 61 SGSGVGTDFLTITISLQFEDFATYYCOQSYSTPQTFGGTKLEIKR 106

RESULT 12
US-08-899-575-105
Sequence 105, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-105

Query Match 86.0%; Score 467; DB 1; Length 107;
Best Local Similarity 86.8%; Pred. No. 4.1e-38;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSLASVGDRTVITSCRASQRIINTYLNWYQHKRGA PKLLIYAASSLSQGVPSRF 60
Db 1 ELTQSPSLASVGDRTVITSCRASQRIINTYLNWYQHKRGA PKLLIYAASSLSQGVPSRF 60

Qy 61 SGSGVGTDFLTITISLQFEDFASYYCOESLSASTYFGGTVEIKR 106
Db 61 SGSGVGTDFLTITISLQFEDFATYYCOQSYSTPQTFGGTKLEIKR 106

RESULT 13
US-08-899-575-105
Sequence 105, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-105

Query Match
Best Local Similarity 86.0%; Score 467; DB 1; Length 107;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 1 ELTQSPSSLSASVGRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60
QY 61 SSGSGVTDFTLTITSSLOFEDPASVYCOESLSASTYTGCGTKVEIKR 106
DB 61 SSGSGGTDPFTLTITSSLOPEDFATVYCOOSYSTPTQTFGQGTKEIKR 106

RESULT 14
PCT-US95-08743-105
Sequence 105, Application PC/TUS9508743

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-105

Query Match
Best Local Similarity 86.0%; Score 467; DB 5; Length 107;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 1 ELTQSPSSLSASVGRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 60
QY 61 SSGSGVTDFTLTITSSLOFEDPASVYCOESLSASTYTGCGTKVEIKR 106
DB 61 SSGSGGTDPFTLTITSSLOPEDFATVYCOOSYSTPTQTFGQGTKEIKR 106

RESULT 15
US-09-240-274-32

Sequence 32, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09396-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 32
LENGTH: 108
TYPE: PRP
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 101
US-09-240-274-32

Query Match
Best Local Similarity 85.5%; Score 464.5; DB 3; Length 108;
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGRVTISCRASQRIINTYLNWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQGVPSRF 61
QY 61 SSGSGVTDFTLTITSSLOFEDPASVYCOESLSA-SYTFGQGTKEIKR 106
DB 62 SSGSGGTDPFTLTITSSLOPEDFATVYCOOSYSTPTPTFGQGTKEIKR 108

Search completed: February 10, 2004, 18:42:08
Job time: 11.9212 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:26:58 ; Search time 10.9212 Seconds

(without alignments)
933.402 Million cell updates/sec

Title: US-10-027-725a-11

Perfect score: 547
Sequence: 1 ELTQSPSSLSASVGDRTVIT.....QOSTTLYTPSGTKLEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR 76:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	468	85.6	108	B49047	Ig kappa chain V r
2	465	85.0	108	S47182	Ig kappa chain - h
3	465	85.0	127	S40367	Ig kappa chain V-J
4	464	84.8	109	S31998	Ig kappa chain - h
5	462	84.5	123	S40331	Ig kappa chain - h
6	457	83.5	122	S40370	Ig kappa chain - h
7	455	83.2	108	S44122	Ig kappa chain V r
8	454	83.0	108	S31977	Ig kappa chain - h
9	453	82.8	129	K1HUMK	Ig kappa chain pre
10	451	82.4	109	S31981	Ig kappa chain - h
11	451	82.4	109	S31978	Ig kappa chain - h
12	449	82.1	108	K1HUMD	Ig kappa chain V-I
13	447	81.7	108	S19674	Ig kappa chain V r
14	446	81.5	129	S40317	Ig kappa chain - h
15	438	80.1	117	S43371	Ig kappa chain V-J
16	437.5	80.0	106	PC2397	anti-tetanus toxin
17	437	79.9	107	S36264	Ig lambda chain V
18	437	79.9	108	K1HUMU	Ig kappa chain V-I
19	437	79.9	120	S46370	Ig kappa chain V-J
20	436	79.7	109	S31979	Ig kappa chain - h
21	434	79.3	129	S52793	Ig kappa chain V r
22	433	79.2	128	S46372	Ig light chain var
23	432	79.0	109	S31980	Ig kappa chain - h
24	432	79.0	125	S40350	Ig kappa chain - h
25	431	78.8	109	S31983	Ig kappa chain - h
26	429	78.4	132	S52792	Ig kappa chain V r
27	429	78.4	129	S40334	Ig kappa chain - h
28	428	78.2	109	S32001	Ig kappa chain - h
29	428	78.2	122	S40314	Ig kappa chain - h

30	428	78.2	132	S38646	Ig kappa chain V r
31	427.5	78.2	125	S40315	Ig kappa chain - h
32	427	78.1	125	S40349	Ig kappa chain V-J
33	425.5	77.8	124	S40336	Ig kappa chain V-J
34	424.5	77.6	107	S36275	Ig kappa chain V
35	424	77.5	108	K1HUMU	Ig kappa chain V-I
36	424	77.5	125	S40333	Ig kappa chain V-J
37	421.5	77.1	108	S30521	Ig kappa chain V r
38	419	76.6	116	A27594	Ig kappa chain pre
39	419	76.6	117	S24206	Ig kappa chain V r
40	418	76.4	109	JN0296	Ig kappa chain V-J
41	418	76.4	129	S40369	Ig kappa chain - h
42	417.5	76.3	108	S34007	Ig kappa chain V r
43	417	76.2	126	S40335	Ig kappa chain V-J
44	416	76.1	108	K1HUMU	Ig kappa chain V-I
45	416	76.1	108	K1HUMK	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

B49047
Ig kappa chain V region (monoclonal strictional autoantibody Strab SA-1A) - human (fragm
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B49047
R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A:Title: Human monoclonal strictional autoantibodies isolated from thymic B lymphocytes
A:Reference number: A49047; PMID:92387224; PMID:1516616
A:Accession: B49047
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-108 <VIC>
A:Experimental source: thymic B lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBI:113208, NCBI:113209)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match Best Local Similarity 85.6%; Score 468; DB 2; Length 108;
Query Similarity 84.9%; Pred. No. 5.7e-36;
Matches 90; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQISITVYNTVQKPKKLLMSASNLQSGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITTCRAQISITVYNTVQKPKKLLIYAAASLQSGVPSRF 62
QY 61 SGSGSGTEFTLTISNLOPEDPASYYCOOSYTTLYTPSGTKLEIKR 106
Db 63 SGSGSGTDFLTITISLQPEDPATYYCOOSYSTPLTFGGTKVEIKR 108

RESULT 2

S47182
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S47182
R:Mcintosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A:Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient
A:Reference number: S47181
A:Accession: S47182
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <MC1>
A:Cross-references: EMBL:X79786; NID:G506422; PIDN:CA56182.1; PID:G506423
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 465; DB 2; Length 108;

62 GSGSGTEFTLTISNLFEDFASYYCQOSTYLLYEGSGKLEIKR 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

C:/Documents and Settings/Administrator/Desktop/06-07-2001
C:/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:/Accession: S44122

A;Note: the sequence was determined from the differentiated gene
C;Genetics:

R. Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. Submitted to the EMBL Data Library, June 1992.

Submitted to the EMBL Data Library, June 1992
A1:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as

Oy 1 ELTOSPSLSASVGDRTTTCRAPOSISTYLNMYOQKPKAKPLITMSASNLQSGVPSRF 60
::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 10 QMTOSPTLSASVGDRTTTCRAPOSISTYLNMYOQKPKAKPLITMSASNLQSGVPSRF 69
Oy 61 SGSGSGTEFTLTISNLQPEDFASYCQ--SYTTLTYFGSGTKLEIKR 106
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 70 SGSGSGTEFTLTISNLQPEDFASYCQYNSYFPPTYFGSGTKLEIKR 117

Search completed: February 10, 2004, 18:41:10
Job time : 10.9212 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 17:48:48 ; Search time 5.94242 Seconds
(without alignments)
838.855 Million cell updates/sec

Title: US-10-027-725A-11

Perfect score: 547

Sequence: 1 ELTQSPSSLSASVGDRTVIT.....QQSYTLYTFSGGKLEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	453	82.8	129	1 KVIW_HUMAN	P04431 homo sapien
2	449	82.1	108	1 KVIK_HUMAN	P01597 homo sapien
3	437	79.9	108	1 KVIN_HUMAN	P01600 homo sapien
4	424	77.5	108	1 KVIN_HUMAN	P01606 homo sapien
5	416	76.1	108	1 KVIK_HUMAN	P01594 homo sapien
6	416	76.1	108	1 KVID_HUMAN	P01607 homo sapien
7	413.5	75.6	107	1 KVID_HUMAN	P01596 homo sapien
8	412	75.3	129	1 KVIK_HUMAN	P04432 homo sapien
9	411.5	75.2	109	1 KVIK_HUMAN	P01612 homo sapien
10	411	75.1	108	1 KVIS_HUMAN	P01611 homo sapien
11	408	74.6	108	1 KVIK_HUMAN	P04430 homo sapien
12	407	74.4	108	1 KVIK_HUMAN	P01598 homo sapien
13	403	73.7	108	1 KVIK_HUMAN	P01608 homo sapien
14	402	73.5	108	1 KVIK_HUMAN	P01593 homo sapien
15	402	73.5	108	1 KVIK_HUMAN	P01599 homo sapien
16	401	73.3	108	1 KVIK_HUMAN	P01604 homo sapien
17	401	73.3	108	1 KVIK_HUMAN	P01602 homo sapien
18	399	72.9	108	1 KVIK_HUMAN	P01595 homo sapien
19	396	72.4	108	1 KVIK_HUMAN	P01610 homo sapien
20	395	72.2	108	1 KVIK_HUMAN	P01603 homo sapien
21	393	71.8	108	1 KVIK_HUMAN	P01609 homo sapien
22	384	70.2	108	1 KVIK_HUMAN	P01605 homo sapien
23	384	70.2	108	1 KVIK_HUMAN	P01606 homo sapien
24	383	70.0	117	1 KVIK_HUMAN	P01602 homo sapien
25	377	68.9	117	1 KVIK_HUMAN	P01601 homo sapien
26	375	68.6	108	1 KVIS_HUMAN	P01647 mus musculu
27	374	68.4	108	1 KVIS_HUMAN	P01644 mus musculu
28	373	68.2	108	1 KVIS_HUMAN	P01636 mus musculu
29	372	68.0	108	1 KVIS_HUMAN	P01645 mus musculu
30	372	68.0	108	1 KVIS_HUMAN	P01652 mus musculu
31	372	68.0	114	1 KVIS_HUMAN	P01625 homo sapien
32	371	67.8	108	1 KVIS_HUMAN	P01648 mus musculu
33	371	67.8	111	1 KVIS_HUMAN	P01665 mus musculu

34	370	67.6	111	1 KVIS_HUMAN	P01667 mus musculu
35	368	67.3	111	1 KVIS_HUMAN	P01664 mus musculu
36	367	67.1	108	1 KVIS_HUMAN	P01649 mus musculu
37	366	66.9	111	1 KVIS_HUMAN	P01669 mus musculu
38	366	66.9	149	1 KVIS_HUMAN	P01634 mus musculu
39	365	66.7	136	1 KVIS_HUMAN	P01634 mus musculu
40	364.5	66.6	129	1 KVIS_HUMAN	P01635 mus musculu
41	363	66.4	108	1 KVIS_HUMAN	P01650 mus musculu
42	362	66.2	111	1 KVIS_HUMAN	P01660 mus musculu
43	362	66.2	111	1 KVIS_HUMAN	P01666 mus musculu
44	362	66.2	134	1 KVIS_HUMAN	P06314 homo sapien
45	361	66.0	108	1 KVIS_HUMAN	P04946 mus musculu

ALIGNMENTS

RESULT 1

ID	KVIW_HUMAN	STANDARD	PRT	129 AA
AC	P04431			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-I region Walker precursor.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85014146; PubMed=6091049;			
RA	Klobeck H.G., Combrato G., Zachau H.G.;			
RT	"Immunoglobulin genes of the kappa light chain type from two human			
RT	lymphoid cell lines are closely related."			
RL	Nucleic Acids Res. 12:6995-7006(1984).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; X00965; CAA25477.1; ALT_TERM.			
DR	PIR; A01883; KIHUMK.			
DR	HSSP; P01607; IREI.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0003823; F:antigen binding activity; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00406; IGV_1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	Immunoglobulin V region; Signal.			
FT	SIGNAL	1	22	IG KAPPA CHAIN V-I REGION WALKER.
FT	CHAIN	23	129	FRAMEWORK-1.
FT	DOMAIN	23	45	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	46	56	COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	57	71	COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN	72	78	COMPLEMENTARITY-DETERMINING-4.
FT	DOMAIN	79	110	FRAMEWORK-2.
FT	DOMAIN	111	119	FRAMEWORK-3.
FT	DOMAIN	120	129	FRAMEWORK-4.
FT	DISULF	45	110	BY SIMILARITY.
FT	NON_TER	129	129	
SQ	SEQUENCE	129 AA;	14069 MW;	P941PA07D4AFC2F9 CRC64;

Query Match 82.8%; Score 453; DB 1; Length 129;
Best Local Similarity 83.8%; Prod. No. 1.4e-40;

Matches 88; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISSTYLNMYOQKPGKAPKLLIWSASNLQSGVPSRF 60
 DB 25 QMTQSPSSLSASVGDRTVITTCRARSISSTYLNMYOQKPGKAPKLLIWSASNLQSGVPSRF 84

QY 61 SSGSGSTEFLLTISNLQFEDFASYYCOOSYTTLYTFGSGTKLEIK 105
 DB 85 SSGSGSTEFLLTISNLQFEDFASYYCOOSYTTLYTFGSGTKLEIK 129

RESULT 2
 KVIH HUMAN STANDARD; PRT; 108 AA.

AC P01597;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 19 kappa chain V-I region DEE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72053133; PubMed=5124396;
 RA Milstein C.P., Deverson E.V.;
 RT "The amino acid sequence of a human kappa light chain."
 RL Biochem. J. 123:945-958 (1971).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR HSSP; P01607; KIHUDE.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_V.
 DR SMART; SM00406; IG_V.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match 82.1%; Score 449; DB 1; Length 108;
 Best Local Similarity 80.2%; Pred. No. 3e-40;
 Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISSTYLNMYOQKPGKAPKLLIWSASNLQSGVPSRF 60
 DB 3 QMTQSPSSLSASVGDRTVITTCRARSISSTYLNMYOQKPGKAPKLLIWSASNLQSGVPSRF 62

QY 61 SSGSGSTEFLLTISNLQFEDFASYYCOOSYTTLYTFGSGTKLEIK 106
 DB 63 SSGSGSTEFLLTISNLQFEDFASYYCOOSYTTLYTFGSGTKLEIK 108

RESULT 3
 KVIH HUMAN STANDARD; PRT; 108 AA.

AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE 19 kappa chain V-I region Hau.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71032830; PubMed=4097974;
 RA Watanabe S., Hillebrand N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups."
 RL Hoppe-Sejler's Z. Physiol. Chem. 351:1291-1295 (1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR HSSP; P80362; IWTU.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_V.
 DR SMART; SM00406; IG_V.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 79.9%; Score 437; DB 1; Length 108;
 Best Local Similarity 78.3%; Pred. No. 5.3e-39;
 Matches 83; Conservative 16; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISSTYLNMYOQKPGKAPKLLIWSASNLQSGVPSRF 60
 DB 3 QMTQSPSSLSASVGDRTVITTCRARSISSTYLNMYOQKPGKAPKLLIWSASNLQSGVPSRF 62

QY 61 SSGSGSTEFLLTISNLQFEDFASYYCOOSYTTLYTFGSGTKLEIK 106
 DB 63 SSGSGSTEFLLTISNLQFEDFASYYCOOSYTTLYTFGSGTKLEIK 108

RESULT 4
 KVIH HUMAN STANDARD; PRT; 108 AA.

AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 19 kappa chain V-I region OU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=70201507; PubMed=5447531;
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
 RT "Macroglobulin structure: variable sequence of light and heavy chains."
 RL Science 169:56-59 (1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.

DR PIR: A01872; KIHUOU.
 DR HSSP: P01607; IREI.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PS50835; IG LINE; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 23. FRAMEWORK-1.
 FT DOMAIN 24 34. COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49. FRAMEWORK-2.
 FT DOMAIN 50 56. COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88. FRAMEWORK-3.
 FT DOMAIN 89 97. COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107. FRAMEWORK-4.
 FT DISULFID 23 88. BY SIMILARITY.
 FT NON_TER 108 108.
 SQ SEQUENCE 108 AA; 11777 MW; 8283DA42A105827E CRC64;
 Query Match 77.5%; Score 424; DB 1; Length 108;
 Best Local Similarity 68.9%; Pred. No. 1,2e-37;
 Matches 73; Conservative 25; Mismatches 8; Indels 0; Gaps 0;
 Oy 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKRGKAPKLLIWSASNIQGVSPSRF 60
 Db 3 QMTZSPSSLSASVGDRTVITTCRAQSISTYLNWYQKRGKAPKLLIWSASNIQGVSPSRF 62
 Oy 61 SGGSGGTFTLTISNLQFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106
 Db 63 SGGSGGTFTLTISNLQFEDFASYYCOQSYTTLTYFGSGTKLEIKR 108
 RESULT 5
 KVI0_HUMAN STANDARD; PRT; 108 AA.
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-I region AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72189444; PubMed=5028201;
 RA Schleich H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 RT protein AU).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehlhauer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the
 RT Bence-Jones protein AU";
 RL Biochem. Struct. Mech. 1:139-146(1975).
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
 CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
 CC REGION OF THE KAPPA CHAIN REI.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 CC PIR: A91653; KIHUOU.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.

DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein; 3d-structure.
 FT DOMAIN 1 23. FRAMEWORK-1.
 FT DOMAIN 24 34. COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49. FRAMEWORK-2.
 FT DOMAIN 50 56. COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88. FRAMEWORK-3.
 FT DOMAIN 89 97. COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107. FRAMEWORK-4.
 FT DISULFID 23 88. BY SIMILARITY.
 FT NON_TER 108 108.
 SQ SEQUENCE 108 AA; 11939 MW; E801187EE6F6B9 CRC64;
 Query Match 76.1%; Score 416; DB 1; Length 108;
 Best Local Similarity 76.4%; Pred. No. 8.4e-37;
 Matches 81; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
 Oy 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKRGKAPKLLIWSASNIQGVSPSRF 60
 Db 3 QMTZSPSSLSASVGDRTVITTCRAQSISTYLNWYQKRGKAPKLLIWSASNIQGVSPSRF 62
 Oy 61 SGGSGGTFTLTISNLQFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106
 Db 63 SGGSGGTFTLTISNLQFEDFASYYCOQSYTTLTYFGSGTKLEIKR 108
 RESULT 6
 KVI0_HUMAN STANDARD; PRT; 108 AA.
 AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-I region Rel.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76023758; PubMed=809329;
 RA Palm W., Hilschmann N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin
 RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
 RT and characterization of the tryptic peptides; the complete amino acid
 RT sequence of the protein; a contribution to the elucidation of the
 RT three-dimensional structure of antibodies, in particular their
 RT combining site";
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=76039968; PubMed=1182131;
 RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
 RT "The molecular structure of a dimer composed of the variable portions
 RT of the Bence-Jones protein REI refined at 2.0-A resolution.";
 RL Biochemistry 14:4943-4952(1975).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 CC PIR: A91653; KIHUOU.
 DR PDB: IAR2; 17-FEB-84.
 DR PDB: IAR2; 12-NOV-97.
 DR PDB: IAR2; 12-NOV-97.
 DR PDB: IAR2; 12-NOV-97.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.

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DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_Like; 1.
DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 FRAMEWORK-2.
FT DOMAIN 35 49 FRAMEWORK-3.
FT DOMAIN 50 56 FRAMEWORK-4.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-4.
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT STRAND 19 25
FT STRAND 30 31
FT STRAND 33 38
FT STRAND 40 41
FT STRAND 44 49
FT STRAND 50 52
FT STRAND 53 54
FT STRAND 56 57
FT STRAND 60 61
FT STRAND 62 67
FT STRAND 68 69
FT STRAND 70 75
FT STRAND 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E118B8CE2A CRC64;

Query Match 76.1%; Score 416; DB 1; Length 108;
Best Local Similarity 75.5%; Pred. No. 8.4e-37;
Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQOSISTYLNWYQKPKKLIWSASNLQGVPSRF 60
DB 3 QMTQSPSTLSASVGDRTVITTCRAQOSIDIKYLNWYQKPKKLIYBASNLQAGVPSRF 62
QY 61 SSGSGSGTEFTLTISNLOFEDFASYYCCQSYYTTLTPGSGTKLEIKR 106
DB 63 SSGSGSGTDYFTLTISNLOFEDFATYYCCQYSLPYTFGGKQITR 108

RESULT 7
ID KVID_HUMAN STANDARD; PRT; 107 AA.
AC P01596;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region CDR.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75075135; Pubmed=4216454;
RA Mlestein C.P.; Deveron E.V.;
RT "Primary structure of kappa light chain from a human myeloma
RT protein."
RL Eur. J. Biochem. 49:377-391(1974).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01864; KIHUAR.
DR HSSP; P80362; IWTU.

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DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0005955; P:immune response; NAS.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_Like; 1.
DR Immunoglobulin V region; Glycoprotein.
FT CARBOHYD 28
FT NON_TER 107
SQ SEQUENCE 107 AA; 11703 MW; E1BFDDF9844C346 CRC64;

Query Match 75.6%; Score 413.5; DB 1; Length 107;
Best Local Similarity 72.6%; Pred. No. 1.5e-36;
Matches 77; Conservative 20; Mismatches 8; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQOSISTYLNWYQKPKKLIWSASNLQGVPSRF 60
DB 3 QMTQSPSTLSASVGDRTVITTCRAQOSISWLNWYQKPKKLIYSSSSLSGVPSRF 62
QY 61 SSGSGSGTEFTLTISNLOFEDFASYYCCQSYYTTLTPGSGTKLEIKR 106
DB 63 SSGSGSGTDYFTLTISNLPBFAFYCCQ-YNPFYFGGKQITR 107

RESULT 8
ID KVID_HUMAN STANDARD; PRT; 129 AA.
AC P04432;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Daudi precursor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; Pubmed=6091049;
RA Kloback H.G.; Combario G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X00966; CAA25478.1; ALT_TERM.
DR PIR; A01884; KIHNDI.
DR HSSP; P80362; IWTU.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0005955; P:immune response; NAS.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_Like; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129
FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
SQ SEQUENCE 129 AA; 14260 MW; 1A1F0D9F844C346 CRC64;

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FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2..
 FT DOMAIN 79 110 FRAMEWORK-3.
 FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 120 129 FRAMEWORK-4.
 FT NON TER 45 110 BY SIMILARITY.
 FT NON TER 129 129
 SQ SEQUENCE 129 AA; 14235 MW; CAF076BCE574C8 CRC64;

Query Match 75.3%; Score 412; DB 1; Length 129;
 Best Local Similarity 74.3%; Pred. No. 2.7e-36;
 Matches 78; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVITTCARQSIISYLMWYQKKGKAPKLLIWSASNLQSGVPSRF 60
 DB 25 QMTQSPSSLSASVGRVITTCAGNITIFLSWYQKKGKATLLIYAVSNLQGVPSRF 84
 QY 61 SGSGSGTEFTLTISNMQEPDPASYYCOOSYTTLYTFSGTGKLEIK 105
 DB 85 SGSGSGAEFTLTISLQPEDPATYFCQAHNVPSFTFGGTTVDIKR 129

RESULT 9

KVLT_HUMAN STANDARD; PRT; 109 AA.
 ID P01612;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ig kappa chain V-I region Mew.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=83081018; PubMed=6616713;
 RA Bultz M., Linke R.P.;

RT "Primary structure of the variable part of an amyloidogenic
 RT Bence-Jones Protein (Mew). An unusual insertion in the third
 RT hypervariable region of a human kappa-immunoglobulin light chain."
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1358 (1982).
 CC -1- MISCELLANEOUS: ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO
 CC FOUND.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A01879; KIHOMV.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein.

KW IMUNOGLOBULIN V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 98 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 99 108 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 109 109
 SQ SEQUENCE 109 AA; 11870 MW; B6ABF451SD55F5A0 CRC64;

Query Match 75.2%; Score 411.5; DB 1; Length 109;
 Best Local Similarity 76.6%; Pred. No. 2.5e-36;
 Matches 82; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 ELTOSPSLSASVGRVITTCARQSIISYLMWYQKKGKAPKLLIWSASNLQSGVPSRF 60
 DB 25 QMTQSPSSLSASVGRVITTCAGNITIFLSWYQKKGKATLLIYAVSNLQGVPSRF 84

DB 3 QMTQSPSSLSASVGRVITTCARQSIISYLMWYQKKGKAPKLLIPTSNIQSGVPSRF 62

QY 61 SGSGSGTEFTLTISNMQEPDPASYYCOOSYTTLYTFSGTGKLEIK 106
 DB 63 SGSGSGTEFTLTISLQPEDPATYFCQAHNVPSFTFGGTTVDIKR 109

RESULT 10

KVLT_HUMAN STANDARD; PRT; 108 AA.
 ID P01611;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Mew.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=81092279; PubMed=6778806;
 RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;

RT "Preparative separation of the tryptic hydrolysate of a protein by
 RT high-pressure liquid chromatography. The primary structure of a
 RT monoclonal L-chain of k-type, subgroup I (Bence-Jones protein
 RT Mew)."
 RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598 (1980).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01877; KIHUMS.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.

KW IMUNOGLOBULIN V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 75.1%; Score 411; DB 1; Length 108;
 Best Local Similarity 74.5%; Pred. No. 2.8e-36;
 Matches 79; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVITTCARQSIISYLMWYQKKGKAPKLLIWSASNLQSGVPSRF 60
 DB 3 QMTQSPSSLSASVGRVITTCAGNITIFLSWYQKKGKATLLIYAVSNLQGVPSRF 62
 QY 61 SGSGSGTEFTLTISNMQEPDPASYYCOOSYTTLYTFSGTGKLEIK 106
 DB 63 SGSGSGTEFTLTISLQPEDPATYFCQAHNVPSFTFGGTTVDIKR 108

RESULT 11

KVLT_HUMAN STANDARD; PRT; 108 AA.
 ID P04430;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region BAN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86174817; PubMed=3083240;
 RA Dwalet F.E., O'Connor T.P., Benson M.D.;
 RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
 RL Mol. Immunol. 23:73-78(1986).
 DR PIR; A01878; KIHUBN.
 DR HSSP; P80362; 1WTU.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; I:1-like.
 DR InterPro; IPR003006; I: MHC.
 DR InterPro; IPR003596; I: V.
 DR Pfam; PF00047; I: 1.
 DR SMART; SM00406; I: 1.
 DR PROSITE; PS0835; I: LIKE; 1.
 DR Immunoglobulin V region; Amyloid.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 FRAMEWORK-4.
 FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 88 FRAMEWORK-4.
 FT NON TER 108 108 BY SIMILARITY.
 SQ SEQUENCE 108 AA; 11840 MW; CD3PD944FE96FD37 CRC64;
 Query Match 74.4%; Score 408; DB 1; Length 108;
 Best Local Similarity 74.5%; Pred. No. 5.8e-36;
 Matches 79; Conservative 12; Mismatches 15; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDRTVITTCARQSIISTYIMWYQKPKAPKLLIWSASNIQGVPSRF 60
 DB 3 QLTQSPSSLSASVGDRTVITTCARQSIISTYIMWYQKPKAPKLLIWSASNIQGVPSRF 62
 QY 61 SSGSGTEFTLTISNLOFEDFASVYCCQSYTYLTLYTFGSGTKLEIKR 106
 DB 63 TSGSGTDFLTITSLQPDPAFYTCQYNSPYTTEGQTKVQIKR 108
 RESULT 12
 KVIP_HUMAN STANDARD; PRT; 108 AA.
 AC P01558;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region EU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71064023; PubMed=5489770;
 RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
 acid sequence of the light chain.";
 RL Biochemistry 9:3155-3161(1970).
 RN [2]
 RP DISULFIDE BOND.
 RX MEDLINE=71064027; PubMed=4923144;
 RA Gali W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 Intra-chain disulfide bonds.";
 RL Biochemistry 9:3188-3196(1970).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A90562; KIHUBU.
 DR HSSP; P01607; IREL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; I:1-like.
 DR InterPro; IPR003006; I: MHC.
 DR InterPro; IPR003596; I: V.
 DR Pfam; PF00047; I: 1.
 DR SMART; SM00406; I: 1.
 DR PROSITE; PS0835; I: LIKE; 1.
 DR Immunoglobulin V region.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 FRAMEWORK-4.
 FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 88 FRAMEWORK-4.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;
 Query Match 74.4%; Score 407; DB 1; Length 108;
 Best Local Similarity 74.3%; Pred. No. 7.3e-36;
 Matches 78; Conservative 15; Mismatches 12; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDRTVITTCARQSIISTYIMWYQKPKAPKLLIWSASNIQGVPSRF 60
 DB 3 QLTQSPSSLSASVGDRTVITTCARQSIISTYIMWYQKPKAPKLLIWSASNIQGVPSRF 62
 QY 61 SSGSGTEFTLTISNLOFEDFASVYCCQSYTYLTLYTFGSGTKLEIKR 105
 DB 63 ISSGSGTEFTLTISNLOFEDFASVYCCQSYTYLTLYTFGSGTKLEIKR 107
 RESULT 13
 KVIP_HUMAN STANDARD; PRT; 108 AA.
 AC P01608;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region ROY.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=68362076; PubMed=5595110;
 RA Hilschmann N.;
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
 Cum.)";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
 RN [2]
 RP REVISIONS TO 39 AND 41.
 RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponatting H.,
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;
 RL (in) Franek F., Shugar D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press,
 New York (1969).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 CC PIR; A91638; KIHURY.
 DR HSSP; P80362; 1WTU.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; I:1-like.


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DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match 73.7%; Score 403; DB 1; Length 108;
Best Local Similarity 72.6%; Pred. No. 1.9e-35;
Matches 77; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTGSPSSLSASVGDVYITTCRARQSIITYLWYQKPKAKLLIWSASNLQGVPSRF 60
DB 3 QMTGSPSSLSASVGDVYITTCQASQDISIFLWYQKPKAKLLIYDASNLQGVPSRF 62
QY 61 SGSGSGTEFTLTISNLQEPDPASYYCOQSYTTLTYFGSGTLEIKR 106
DB 63 SGSGGTEFTLTISNLQEPDPATYYCOQFDNLPLTFGGGTKEVDFKR 108

RESULT 14
KV1A_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969). THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR HSSP: P01607; IREI.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG_1-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 FRAMEWORK-4.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

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Query Match 73.5%; Score 402; DB 1; Length 108;
Best Local Similarity 74.5%; Pred. No. 2.4e-35;
Matches 79; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 ELTGSPSSLSASVGDVYITTCRARQSIITYLWYQKPKAKLLIWSASNLQGVPSRF 60
DB 3 QMTGSPSSLSASVGDVYITTCQASQDISIFLWYQKPKAKLLIYDASNLQGVPSRF 62
QY 61 SGSGSGTEFTLTISNLQEPDPASYYCOQSYTTLTYFGSGTLEIKR 106
DB 63 SGSGGTEFTLTISNLQEPDPATYYCOQFDNLPLTFGGGTKEVDFKR 108

RESULT 15
KV1G_HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Gal.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IGM-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR: A01867; KIHUGL.
DR HSSP: P01607; IREI.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding activity; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG_1-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match 73.5%; Score 402; DB 1; Length 108;
Best Local Similarity 75.5%; Pred. No. 2.4e-35;
Matches 80; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTGSPSSLSASVGDVYITTCRARQSIITYLWYQKPKAKLLIWSASNLQGVPSRF 60
DB 3 QMTGSPSSLSASVGDVYITTCQASQDISIFLWYQKPKAKLLIYDASNLQGVPSRF 62
QY 61 SGSGSGTEFTLTISNLQEPDPASYYCOQSYTTLTYFGSGTLEIKR 106
DB 63 SGSGGTEFTLTISNLQEPDPATYYCOQFDNLPLTFGGGTKEVDFKR 108

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Search completed: February 10, 2004, 18:36:31
Job time : 5.94242 secs

Db 3 QMTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPNLIYAASLSQGVPSRF 62
QY 61 SSGSGSTEFTLTISNLOFEDFASYYCCOQSYTTLTYTGGSKLEIKR 106
DB 63 SSGSGSTDFTLTISLQPEDFATYYCCQSYSTSWTGTGKVEIKR 108

RESULT 2
Q96SA9
ID Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE Variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RP MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 85.1%; Score 465.5; DB 4; Length 107;
Best Local Similarity 85.8%; Pred. No. 2.4e-44;
Matches 91; Conservative 11; Mismatches 3; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPNLIYAASLSQGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPNLIYAASLSQGVPSRF 62

QY 61 SSGSGSTEFTLTISNLOFEDFASYYCCOQSYTTLTYTGGSKLEIKR 106
DB 63 SSGSGSTDFTLTISLQPEDFATYYCCQSYSTL-TGCGTKVEIKR 107

RESULT 3
Q9UL81
ID Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035033; AAD56269.1; -
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 82.0%; Score 448.5; DB 4; Length 107;
Best Local Similarity 82.1%; Pred. No. 1.9e-42;
Matches 87; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPNLIYAASLSQGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPNLIYAASLSQGVPSRF 62

QY 61 SSGSGSTEFTLTISNLOFEDFASYYCCOQSYTTLTYTGGSKLEIKR 106
DB 63 SSGSGSTDFTLTISLQPEDFATYYCCQSYSTL-TFGPKVDIKR 107

RESULT 4
Q9UL70
ID Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RP MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 75.7%; Score 414; DB 4; Length 108;
Best Local Similarity 77.4%; Pred. No. 1.4e-38;
Matches 82; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPNLIYAASLSQGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQKPGKAPNLIYAASLSQGVPSRF 62

QY 61 SSGSGSTEFTLTISNLOFEDFASYYCCOQSYTTLTYTGGSKLEIKR 106
DB 63 SSGSGSTDFTLTISLQPEDFATYYCCQKNSAPRTFGKLEIKR 108

RESULT 5
Q9UL79

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ID Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 75.5%; Score 413; DB 4; Length 108;
Best Local Similarity 77.1%; Pred. No. 1.8e-38;
Matches 81; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITCRAROSISTYINWYQOKRGKAPKLLIWSASNLQSGVPSRF 61
DB 4 MTQSPSLASASGDRVTISCRASQGISSTLANWYQOKRGKAPKLLIWSASNLQSGVPSRF 63
QY 62 GSGSGTEFTLTISNLOFEDFASYYCOQSYTTLYTFGSGTKLEIKR 106
DB 64 GSGSGTDFLTISNLOFEDFATYYCQQYSPPTFGGKTKVEIKR 108

RESULT 6
Q9QYFO PRELIMINARY; PRT; 298 AA.
AC Q9QYFO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CN 8 scFv.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=20183931; PubMed=10706631;
RA Shiohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phase display subtraction
RT method."
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR EMBL; AB036341; BAA8633.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 2.
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DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 70.7%; Score 387; DB 11; Length 298;
Best Local Similarity 69.8%; Pred. No. 5.1e-35;
Matches 74; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRAROSISTYINWYQOKRGKAPKLLIWSASNLQSGVPSRF 60
DB 175 ELTQSPSLASASVGEVITTCRAGSNINHWYQOKGSPKLLIWSASNLQSGVPSRF 234
QY 61 GSGSGTEFTLTISNLOFEDFASYYCOQSYTTLYTFGSGTKLEIKR 106
DB 225 GSGSGTGYSLKINSLOPEDFGSYCQHFMTTPTFGGKTKLEIKR 280

RESULT 7
Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Struhsberg R.;
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6B7812D2 CRC64;

Query Match 69.3%; Score 379; DB 11; Length 234;
Best Local Similarity 68.9%; Pred. No. 2.9e-34;
Matches 73; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRAROSISTYINWYQOKRGKAPKLLIWSASNLQSGVPSRF 60
DB 23 QMTQTSLSASLSDGRVTISCRASODISNHWYQOKRGKAPKLLIWSASNLQSGVPSRF 82
QY 61 GSGSGTEFTLTISNLOFEDFASYYCOQSYTTLYTFGSGTKLEIKR 106
DB 83 GSGSGTGYSLKINSLOPEDFGSYCQHFMTTPTFGGKTKLEIKR 128

RESULT 8
Q96PF6 PRELIMINARY; PRT; 116 AA.
AC Q96PF6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Kappa 1 light chain variable region (Fragment).
GN SGNL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
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[illegible]

ID	Q9R062	PRELIMINARY;	PRT;	234 AA.
AC	Q9R062.			
DT	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Hypothetical 25.9 kDa protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
OX	NCBI_taxid=10090;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Colon;			
RA	Strasbourg R.;			
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC027418: AAH27418.1: -			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_V.			
DR	Pfam; PF00047; IG_2.			
DR	SMART; SM00406; IGV_1.			
DR	PROSITE; PS00835; IG_LIKE; 2.			
DR	PROSITE; PS00290; IG_MHC; 1.			
KW	Hypothetical protein.			
SO	SEQUENCE 234 AA; 25857 MW; 4EB08C81426AAB1 CRC64;			
Query Match		68.4%;	Score 374;	DB 11; Length 234;
Best Local Similarity		69.8%;	Pred. No. 1.1e-33;	
Matches 74;	Conservative 12;	Mismatches 20;	Indels 0;	Gaps 0;
QY	1 ELTQSPSSLSAVGRRVITTCRAPQISITLTYNMVOOKGKAKPLIWSASNIQSGVPSRF 60			
DB	23 QMTQTSSLSLGGKRVITISCSAGSISNLMWVOOKPDDGVTKLIYTTSLHSGVPSRF 82			
QY	61 SGGSGTEFTLTISNLQEPFASVYCCQSYTTLTYFGSGTKLEIKR 106			
DB	83 SGGSGGTHYSLTISNLPEPDIATVYCCQYSGPFPFGSGTKLEIKR 128			
RESULT 10				
Q920E6		PRELIMINARY;	PRT;	109 AA.
ID	Q920E6			

AC Q920E6; 2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)
DE Pefrin-mimicking anti-idiotope kappa chain variable region
DE (Fragment).
DE OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pefrin-Mimicking Antibodies Expressed
in Mamalian Cells";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307818; AA009422.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
PF Pfam; PF00047; IG; 1.
SM SMART; SMO0406; IGv; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1_1
FT TER 109
SQ SEQUENCE 109 AA; 11943 MW; DAD3F98BE05DD1501 CRC64;

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Query Match      68.2%; Score 373; DB 11; Length 109;
Beat Local Similarity    66.0%; Pred. No. 5.3e-34;
Matches 70; Conservative 18; Mismatches 18; Indels 0; Gaps 0

Qy      1 ELTSPSSLSASVGDYRTITCTCRARQSISTYLWNYOQRGKAPKLILWSASNIQGVPSRF 60
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      3 QMTGSFSLASVGETVTITCRASGINHNLYLAWYOQRGSKPQLLVYAKTLADGVPSRF 62
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy      61 SGGSSGTETFTLTISNLOPEDPASYYCOOSYTLLTFSGSTLEIKR 106
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      63 SGGSSGTGYSLKINSIQPEDFGSYCYHFWSTPWTFFGGTXLEIKR 108
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 11
Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TREMBLrel_13, Created)
DT 01-MAY-2000 (TREMBLrel_13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel_23, Last annotation update)
DE Myosin-reactive Immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
   Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR HSSP; P80362; IWL.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9CEA92EBB96EEA CRC64;
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DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AH13496.1; -.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KM Hypothetical protein.
FT NON_TER
SQ
SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 66.5%; Score 364; DB 11; Length 233;
Best Local Similarity 67.0%; Pred. No. 1,4e-32;
Matches 71; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQISISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
DB :||:||||:||||:|:|||||||:|||||||:|||||||:|||||||:|||||||:
22 QMTQTTSLSASLGDRTVITCSGSGGIANYLNWYQOKPDGTVKLLIYTTSSLHSGVPSRF 81
QY 61 SSGSGGTEFTLTISNLFEDFASVYCCOQSYTTLTYFGSGTKLEIKR 106
DB |||||:||||:||||:|:|||||||:|||||||:|||||||:|||||||:
82 SSGSGGTDVSLTISNLEPDIAIYCCOQRYRLPMTFGGTKLEIKR 127

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 Job time : 26.0545 secs

XX	FN	MO200253595-A1.
XX	FD	11-JUL-2002.
XX	PF	27-DEC-2001; 2001WO-SE02908.
XX	PR	29-DEC-2000; 2000SE-0004892.
XX	PA	(PHAA) PHARMACIA DIAGNOSTICS AB.
XX	PI	Flicker S, Steinberger P, Kraft D, Valenta R;
XX	PI	WPI: 2002-583604/62.
XX	DR	N-PSDB; ABK89641.
XX	PT	Group 2 allergen-specific immunoglobulins (Ig) E Fabs or Igg comprising
XX	PT	variable region of group 2 allergen specific-human IGE Fabs, useful for
XX	PT	diagnosing or passive immunotherapy of type I allergy, for
XX	PT	environmental allergen detection -
XX	PS	Disclosure; Page 40; 45pp; English.
XX	CC	This invention relates to the DNA and protein sequences of group 2
XX	CC	allergen-specific human IGE Fabs and methods for their use. The proteins
XX	CC	of the invention may have antiallergic activities and may be used as a
XX	CC	vaccine or an inhibitor of binding of grass pollen allergic patient's
XX	CC	IGE antibodies to Phi P 2 (a major Timothy grass pollen allergen).
XX	CC	The group 2 allergen-specific Fabs of the invention may be useful for
XX	CC	environmental allergen detection and for standardisation of allergen
XX	CC	extracts. The Fabs - or a vaccine against a type I allergy is useful for
XX	CC	passive immunotherapy of type I allergy, it is also useful for
XX	CC	diagnosing a type I allergy. The allergen-specific Fabs of the invention
XX	CC	are useful for inter alia, diagnosis, therapy and prevention of type
XX	CC	I allergy. They are also useful for identification of group 2
XX	CC	allergen-containing pollen and may be used for blocking the binding of
XX	CC	grass pollen allergic patients IGE antibodies to Phi P 2. The present
XX	CC	sequence represents the human IGE fab, clone 60 light chain protein of
XX	CC	the invention.
XX	SO	Sequence 106 AA;
XX	SO	Query Match 98.2%; Score 537; DB 23; Length 106;
XX	SO	Best Local Similarity 99.1%; Pred. No. 2,4e-30;
XX	SO	Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps
XX	OY	1 ELTQPSPLSLASVGDRTVITICRAROSISTYLNMYQOKPGKAPKLLIMSNLQSGVPSRF 60
XX	DB	1 ELTQPSPLSLASVGDRTVITICRAROSISTYLNMYQOKPGKAPKLLIMSNLQSGVPSRF 60
XX	OY	61 SGSSGTEFTLTITSNLQFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106
XX	DB	61 SGSSGTEFTLTITSNLQFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106
XX	RESULT 2	
XX	ID	AAR54260 AAR54260 standard; protein; 107 AA.
XX	AC	AAR54260;
XX	DT	25-MAR-2003 (updated)
XX	DT	10-NOV-1994 (first entry)
XX	DE	Anti-HIV gp120 immunoglobulin light chain variable region b22.
XX	KW	Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
XX	KW	neutralisation; monoclonal antibody; kappa light chain;
XX	KW	variable region; framework; complementarity determining region.
XX	OS	Homo sapiens.
XX	XX	
XX	Key	Location/Qualifiers

FT	Region		1..21	/label= FR1
FT	Region		22..33	/label= CDR1
FT	Region		34..48	/label= FR2
FT	Region		49..55	/label= CDR2
FT	Region		56..87	/label= FR3
FT	Region		88..95	/label= CDR3
FT	Region		96..107	/label= FR4
XX				
PV	WO9407922-A1.			
PD	14-APR-1994.			
PP	30-SEP-1993;	93WO-US09328.		
PR	30-SEP-1992;	92US-0954148.		
PA	(SCRI) SCRIPPS RES INST.			
PI	Barbas CF, Burton DR, Lerner RA;			
XX				
DR	WPI; 1994-135516/16.			
PT	New human monoclonal antibodies neutralising HIV - react with gp120 or gp41 and nucleic acid encoding them, useful for in vivo or in vitro diagnosis and for passive immuno-therapy			
XX				
PS	Claim 5; Page 189; 248pp; English.			
CC	Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification using primers specific for heavy and light chain variable regions. The amplification products were inserted into a distictronic vector to produce a library of fragments. E.coli XL1 Blue cells were transformed with the library. Filamentous phage were produced which expressed the MAb regions on their surface. Panning with gp120 and gp41 resulted in the recovery of immunoreactive clones. The light chain VK region sequence AARS4260 neutralises HIV1 gp120.			
CC	(Updated on 25-MAR-2003 to correct PN field.)			
SQ	Sequence 107 AA;			
	Query Match 88.5%; Score 484; DB 15; Length 107; Best Local Similarity 88.7%; Pred. No. 1.le-26; Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0			
OY	1 ELTOSPSLSASVGGRVTITTCRAROSISTYLNMTYQQKPKAKPLTIWSASNLOSVPSPRF 60 :			
Ddb	1 ELTOSPSLSASVGDRVTITTCRASGISISYLNMTYQQKKGKPKLLIYAASSLQSGVSPSRF 60 :			
OY	61 SGGSGTEFTLTISNLOFEDEASYYYCQGSYTTLTYFGSGTKLEIKR 106 :			
Ddb	61 SGGSGTDFTLTISLQPEDEPATYCYCQGSYSTPTTFGCGTKLEIKR 106 :			
RESULT 3				
ID	AAW01283 standard; Protein; 107 AA.			
AC	AAW01283;			
DT	29-JAN-1997 (first entry)			
DE	VL region of HIV neutralising MAb, clone b22 and B35.			
KM	Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;			

```

KW virus infectivity assay; precursor gp160; immunocompetence; human;
KV anti-HIV antibody; detection; HIV infection.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Region 1..21
FT /label= FR1
FT Region 22..32
FT /label= CDR1
FT Region 33..47
FT /label= FR2
FT Region 48..54
FT /label= CDR2
FT Region 55..86
FT /label= FR3
FT Region 87..95
FT /label= CDR3
FT Region 96..107
FT /label= FR4
XX
XX WO9602273-A1.
XX PD 01-FEB-1996.
XX PF 11-JUL-1995; 95WO-US08743.
XX PR 18-JUL-1994; 94US-0276852.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Barbas CF, Burton DR, Lerner RA;
XX DR WPI, 1996-179601/18.
XX PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in
PT passive immuno:therapy and detection of HIV infection.
XX
XX Example; Fig 11; 366pp; English.
XX
XX The sequences given in AAM01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (Mab's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK2
CC gene clones, b22 and B35. A Mab containing this VL sequence has the
CC capacity to reduce HIV infectivity titre in an in vivo virus
CC infectivity assay by 50 % at a concentration of less than 700 ng
CC of antibody/ml, and binds mature gp120 preferentially over the
CC precursor gp160. The Mab may be used for determining immunocompetence
CC of a human anti-HIV antibody and in the detection of HIV infection.
CC
SQ Sequence 107 AA;
XX
XX Query Match 88.5%; Score 484; DB 17; Length 107;
XX Best Local Similarity 88.7%; Pred. No. 1.le-26;
XX Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0.
XX
QY 1 ELTSPSSISASVGRVTITTCARASISTYLNMWYOOKPKAPKLIWSASNLSGVPSRF 60
Db 1 ELTSPSSISASVGRVTITTCARASISSIYLMWYOKPEKAKLIIAASSLSQGVPSRF 60
| | | | | | | | | | | | | | | | | | | | | | : | | | | |
QY 61 SSGSGTEFTLTISM,QEEDFASYCOOSYTYLLYTFGSGTKLEIKR 106
Db 61 SSGSGCTDFTLTISLQPEDFAFYCQGSYSPIPYFGGQTKLEIKR 106
| | | | | | | | | | | | | | | | | | | | | | | | | | |
RESULT 4
ID AAY95135 standard; Protein; 107 AA.
AC AAY95135;
XX
DT 30-JUN-2000 (first entry)

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DE      Anti-gp120 antibody light chain variable region from clone b22.
XX
XX      Anti-human immunodeficiency virus type 1 antibody; HIV-1, neutralise;
XX      reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
XX      glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
XX
XX      Homo sapiens.
XX
XX      AU9948756-A.
XX
XX      17-FEB-2000.
XX
XX      16-SEP-1999; 99AU-0048756.
XX
XX      16-SEP-1999; 99AU-0048756.
XX
XX      (SCRI ) SCRIPPS RES INST.
XX
XX      Burton DR, Barbas CF, Lerner RA;
XX
XX      WPI; 2000-293393/26.
XX
XX      Novel human monoclonal antibodies which immunoreact with and neutralise
XX      human immunodeficiency virus useful for treating HIV infections
XX
XX      Example 9; Figure 11; 36pp; English.
XX
XX      The present sequence represents a fragment of an anti-human
XX      immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
XX      a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
XX      mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
XX      gp160 and neutralises HIV and which reduces HIV infectivity titre in an
XX      in vitro virus infectivity assay by 50%, at a concentration of less than
XX      700 ng/ml. The antibodies are used as reagents for the diagnosis and
XX      immunotherapy of HIV induced disease. They are useful as neutralising
XX      field isolates and provide useful information regarding the
XX      immunocompetence of an immune response in HIV infected patients. The
XX      monoclonal antibodies are useful for producing anti-idiotypic antibodies
XX      which can be used to screen human monoclonal antibodies to identify
XX      whether the antibody has the same binding specificity as the antibodies
XX      of the invention. The neutralising antibodies define new epitopes on the
XX      HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
XX      immunotherapeutic human monoclonal antibodies. A major advantages of the
XX      monoclonal antibodies derives from the fact that they are encoded by a
XX      human polynucleotide sequence. Thus in vivo use of the monoclonal
XX      antibodies for diagnosis and immunotherapy of HIV induced disease greatly
XX      reduces the problems of significant host immune response to the passively
XX      administered antibodies which is a problem commonly encountered when
XX      monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
XX      An additional major advantage of the monoclonal antibodies described
XX      derives from the fact that they immunoreact with a unique determinant
XX      present on mature HIV glycoprotein gp120. This class of antibodies is
XX      particularly effective at neutralising field isolates of HIV.
XX
XX      Sequence 107 AA;
XX
XX      Query Match 88.5%; Score 484; DB 21; Length 107;
XX      Best Local Similarity 88.7%; Pred. No. 1,1e-26;
XX      Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0
XX
XX      1 ELTQSPSSLSASVGDRTVITTCRAQGISITYLNMVQQRKGAKPKLLIWSASNIQGVPSRF 60
XX      1 ELTQSPSSLSASVGDRTVITTCRAQGISISSYLNWVQQRKGAKPKLLIYASISQGVPSRF 60
XX
XX      61 SGSSSGTEFTLTITSLNQLQEPDPAASYCOOSYTLTLTFFSGGTGLAIKR 106
XX      61 SGSSSGTEFTLTITSLNQLQEPDPAASYCOOSYTLTLTFFSGGTGLAIKR 106
XX
XX      61 SGSSSGTDFTLTITSLQPEDFATYCCOOSYSTPTFFGGTGLAIKR 106
XX
XX      RESULT 5
XX      AAY98244
XX      AAY98244 standard; Protein: 107 AA.

```

XX AAY98244;
 AC 04-UTL-2000 (first entry)
 DT 04-UTL-2000 (first entry)
 DE Anti-gp120 antibody light chain variable region from clone b22.
 XX
 XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KM human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KM passive immunotherapy; reduce severity; HIV-induced disease;
 KM immunocompetence; active immunisation.
 OS Homo sapiens.
 XX
 XX AU9948754-A.
 PN 17-FEB-2000.
 PD 16-SEP-1999; 99AU-0048754.
 PF 16-SEP-1999; 99AU-0048754.
 XX 16-SEP-1999; 99AU-0048754.
 PR (SCRI) SCRIPPS RES INST.
 PA Burton DR, Barbas CF, Lerner RA;
 PI WPI; 2000-246867/22.
 DR Human neutralizing monoclonal antibodies to human immunodeficiency
 PT virus (HIV) used for providing passive immunotherapy to HIV are
 PT specific for glycoprotein-120 -
 XX
 XX Example 9; Figure 11; 374pp; English.
 PS This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody
 CC capable of reducing an HIV infectivity titre in an in vitro virus
 CC infectivity assay by 50% at a concentration of less than 70 ng/ml. The
 CC method for the production of the antibody comprises:
 CC (a) providing a first polynucleotide encoding a heavy chain
 CC immunoglobulin amino acid sequence (which does not comprise the sequence
 CC represented by AAY98206) and a second polynucleotide encoding a light
 CC chain immunoglobulin amino acid sequence;
 CC (b) inserting the first and second polynucleotide sequences into a host
 CC cell;
 CC (c) maintaining the host cell in conditions which allow the amino acid
 CC sequences encoded by the polynucleotides to be expressed in the host
 CC cell; and
 CC (d) isolating the antibody comprising the heavy and light chain
 CC immunoglobulin amino acid sequences from the host cell.
 CC The anti-HIV gp-120 monoclonal antibody is used for providing passive
 CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used
 CC for neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting
 CC HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the
 CC antibodies associated with monoclonal antibodies of xenogeneic or
 CC chimeric derivation.
 XX
 XX Sequence 107 AA;

Query Match 88.5%; Score 484; DB 21; Length 107;
 Best Local Similarity 88.7%; Pred. No. 1.1e-26;

Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGRVITTCAROSISITLWYQOKPEKAPKLIMSASNTQSGVPSRF 60
 DB 1 ELTQSPSSLSASVGRVITTCAROSISITLWYQOKPEKAPKLIMSASNTQSGVPSRF 60
 QY 61 SSGSGCTEFTLTISNLOFEDFASVYCCOQSYTTLTYFGSGTKLEIKR 106
 DB 61 SSGSGCTEFTLTISNLOFEDFATYCCOQSYTTLTYFGSGTKLEIKR 106
 RESULT 6
 AAG93590
 ID AAG93590 standard; Protein; 107 AA.
 AC AAG93590;
 XX
 XX 14-SEP-2001 (first entry)
 DT 14-SEP-2001 (first entry)
 DE Human anti-Rh(D) chain I02 protein sequence.
 XX
 XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KM red blood cell; Rh phenotype; diagnosis; therapeutic.
 OS Homo sapiens.
 XX
 XX US6255455-B1.
 PN 03-JUL-2001.
 PD 29-JAN-1999; 99US-0240274.
 PF 11-OCT-1996; 96US-0028550.
 PR 10-APR-1998; 98US-0081380.
 PR 27-JUN-1997; 97US-0884045.
 XX
 XX (UYPR-) UNIV PENNSYLVANIA.
 PA
 PI Stegel DL;
 DR N-PDB; AAG68647.
 DR N-PDB; AAG68647.
 PS New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine -
 XX
 XX Claim 1; Column 43; 162pp; English.
 PS
 CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAG68615 to AAG68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.
 XX
 XX Sequence 107 AA;

Query Match 88.3%; Score 483; DB 22; Length 107;
 Best Local Similarity 87.7%; Pred. No. 1.3e-26;
 Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGRVITTCAROSISITLWYQOKPEKAPKLIMSASNTQSGVPSRF 60
 DB 2 ELTQSPSSLSASVGRVITTCAROSISITLWYQOKPEKAPKLIMSASNTQSGVPSRF 61
 QY 61 SSGSGCTEFTLTISNLOFEDFASVYCCOQSYTTLTYFGSGTKLEIKR 106
 DB 61 SSGSGCTEFTLTISNLOFEDFATYCCOQSYTTLTYFGSGTKLEIKR 106

Db 62 SSGSGTDTFTLTISLQPEDFATYCCQSYSTLMTFGGKTKEIKR 107

RESULT 7

AAG3644 ID AAG3644 standard; Protein; 107 AA.

AC AAG3644;

DT 14-SEP-2001 (first entry)

XX Human anti-Rh(D) antibody clone SH13 protein sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;

KM red blood cell; Rh phenotype; diagnosis; therapeutic.

XX Homo sapiens.

XX US6255455-B1.

XX 03-JUL-2001.

XX 29-JAN-1999; 99US-0240274.

XX 11-OCT-1996; 96US-0028550.

XX 10-APR-1998; 98US-0081380.

XX 27-JUN-1997; 97US-0884045.

XX (UNPE-) UNIV PENNSYLVANIA.

XX Siegel DL;

XX WPI; 2001-388931/41.

XX N-PSDB; AAH68701.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in

XX diagnostics requiring a human instead of an animal antibody and in

XX therapeutic medicine -

XX Claim 1; Column 68; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,

XX preferably a human antibody, (I) having an amino acid sequence comprising

XX one of the sequences (S) given in AAG3644 to AAG3669. (I) has

XX immunostimulant activity, and can be used as an immune system stimulant.

XX (I) can be used in diagnostic and therapeutic medicine. The antibodies

XX are used in diagnostics that require human antibodies instead of animal

XX antibodies, such as determine the Rh phenotype of human red blood cells.

XX AAH68615 to AAH68726 represent the nucleotide sequence which encode

XX AAG3658 to AAG3669, AAG3670 to AAG3697 represent anti-Rh(D) heavy

XX chain CDR3 amino acid sequences which are given in the exemplification

XX of the present invention.

XX Sequence 107 AA;

XX SQ

Query Match 87.8%; Score 480; DB 22; Length 107;
Best Local Similarity 87.7%; Fred. No. 2.1e-26;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVTITTCAROSISTYLNWYQOKPKKLIWSASNLQSGVPSRF 60
DB 2 ELTOSPSLSASVGRVTITTCAROSISTYLNWYQOKPKKLIWSASNLQSGVPSRF 61
QY 61 SSGSGTEFTLTISNLQPEDFASYCCQSYSTLTLYTFSGKTKEIKR 106
DB 62 SSGSGTDTFTLTISLQPEDFATYCCQSYSTLTLYTFSGKTKEIKR 107

RESULT 8

AAR54261 ID AAR54261 standard; protein; 107 AA.

AC AAR54261;

XX 25-MAR-2003 (updated)
DT 10-NOV-1994 (first entry)

XX Anti-HIV gp120 immunoglobulin light chain variable region b27.

XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;

KM neutralisation; monoclonal antibody; kappa light chain;

XX variable region; framework; complementarity determining region.

XX Homo sapiens.

XX Key

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

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XX Region

XX Region

XX Region

XX Region

XX Region

XX Region

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XX Region

XX Region

Query Match 87.0%; Score 476; DB 15; Length 107;
Best Local Similarity 87.7%; Fred. No. 4.1e-26;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVTITTCAROSISTYLNWYQOKPKKLIWSASNLQSGVPSRF 60
DB 1 ELTOSPSLSASVGRVTITTCAROSISTYLNWYQOKPKKLIWSASNLQSGVPSRF 60
QY 61 SSGSGTEFTLTISNLQPEDFASYCCQSYSTLTLYTFSGKTKEIKR 106
DB 61 SSGSGTDTFTLTISLQPEDFATYCCQSYSTLTLYTFSGKTKEIKR 106

RESULT 9

AAR54261 ID AAR54261 standard; protein; 107 AA.

AC AAR54261;

	RESULT 9	
ID	AAM01284	AAM01284 standard; Protein; 107 AA.
XX AC	AAM01284;	
DT DT	29-JAN-1997	(first entry)
DB XX	VL region of HIV neutralising Mab, clone b27.	
KW KW	Heavy chain; light chain; variable region; VH; monoclonal antibody; MAB; HIV; human immunodeficiency virus; glycoprotein; gp120; clone; virus infectivity assay; precursor gp160; immunocompetence; human; anti-HIV antibody; detection; HIV infection.	
OS XX	Homo sapiens.	
Key Key	Location/Qualifiers	
FH FT	1..21 /label= FR1	
FT FT	Region Region	22..32 /label= CDR1
FT FT	Region Region	33..47 /label= FR2
FT FT	Region Region	48..54 /label= CDR2
FT FT	Region Region	55..86 /label= FR3
FT FT	Region Region	87..95 /label= CDR3
FT FT	Region Region	96..107 /label= FR4
PN PN	WO9602273-AI.	
PD PD	01-FEB-1996.	
PF PF	11-JUL-1995; 95WO-US08743.	
PR PR	18-JUL-1994; 94US-0276852.	
PA PA	(SCRI) SCRIPPS RES INST.	
PI PI	Bardas CF, Burton DR, Lerner RA;	
DR DR	WPI, 1996-179601/18.	
PT PT	Monoclonal antibody binding to VI/V2 loop of HIV gp120 - used in passive immuno-therapy and detection of HIV infection.	
PS PS	Example; Fig 11; 366pp; English.	
CC CC	The sequences given in AAM01261-92 represent the light chain variable regions (VL) of a series of monoclonal antibodies (Mab's) which are immunoreactive with HIV glycoprotein gp120 and are capable of neutralising HIV. This sequence represents the sequence of the JK2 gene clone, b27. A Mab containing this VL sequence has the capacity to reduce HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a concentration of less than 700 ng of antibody/mL, and binds mature gp120 preferentially over the precursor gp160. The Mab may be used for determining immunocompetence of a human anti-HIV antibody and in the detection of HIV infection.	
SQ SQ	Sequence 107 AA;	
Query Match	87.0%; Score 476; DB 17; Length 107;	
Best Local Similarity	87.7%; Pred. No. 4.1e-26;	
Matches	93; Conservative 8; Mismatches 5; Indels 0; Gaps 0	
DG	1 ELTGPPSSLSASVGRVTITTCARAGSISYILMWYOOKPKAKRLIMASNIGCVPRF 60	
DB	1 ELTGPSPSSLSASVGRTVVTTTCAASGISISSYLWMYOOPKAPKAFLIYAASSIQGVPRF 60	

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Oy      61  SGGSSGTEFTLTINLQEPFASYYCOOSYTTLTTFSSGTLLEIKR 106
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      61  SGGSSGDTFTLTISLQEPDPATYYCOOSYSTPTPFQGTLEIKR 106

RESULT 10
ID      AAY95136
AA      AAY95136 standard; Protein; 107 AA.
AC      AAY95136;
AD
AE
AF
AG      30-JUN-2000 (first entry)
AH
AI
AJ
AK      Anti-gp120 antibody light chain variable region from clone B27.
AL
AM
AN
AO
AP      Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
AQ      reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
AR      glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
AS
AT      Homo sapiens.
AU
AV      AU9948756-A.
AW
AX      17-FEB-2000.
AY
AZ      16-SEP-1999; 99AU-0048756.
BA      16-SEP-1999; 99AU-0048756.
BB
BC      (SCRI ) SCRIPPS RES INST.
BD
BE      Burton DR, Barbas CF, Lerner RA;
BF      WPI; 2000-293393/26.
BG
BH
BI      Novel human monoclonal antibodies which immunoreact with and neutralise
BJ      human immunodeficiency virus useful for treating HIV infections
BK
BL      Example 9; Figure 11; 366pp; English.
BM
BN
BO
BP      The present sequence represents a fragment of an anti-human
BQ      immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
BR      a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
BS      mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
BT      gp160 and neutralises HIV and which reduces HIV infectivity titre in an
BV      in vitro virus infectivity assay by 50% at a concentration of less than
BW      700 ng/ml. The antibodies are used as reagents for the diagnosis and
BX      immunotherapy of HIV induced disease. They are useful as neutralising
BY      field isolates and provide useful information regarding the
BZ      immunocompetence of an immune response in HIV infected patients. The
CA      monoclonal antibodies are useful for producing anti-idiotypic antibodies
CB      which can be used to screen human monoclonal antibodies to identify
CC      whether the antibody has the same binding specificity as the antibodies
CD      of the invention. The neutralising antibodies define new epitopes on the
CE      HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
CF      immunotherapeutic human monoclonal antibodies. A major advantages of the
CG      monoclonal antibodies derives from the fact that they are encoded by a
CH      human polynucleotide sequence. Thus in vivo use of the monoclonal
CI      antibodies for diagnosis and immunotherapy of HIV induced disease greatly
CJ      reduces the problems of significant host immune response to the passively
CK      administered antibodies which is a problem commonly encountered when
CL      monoclonal antibodies of xenogenic or chimeric derivation are utilized.
CM      An additional major advantage of the monoclonal antibodies described
CN      derives from the fact that they immunoreact with a unique determinant
CO      present on mature HIV glycoprotein gp120. This class of antibodies is
CP      particularly effective at neutralising field isolates of HIV.
CQ
CR
CS
CT      Sequence 107 AA;
CU
CV
CW
CX
CY
CZ

```

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISTYINMWYQKRGKAPKLLIMSASNLQSGVPSRF 60
 DB 1 ELTQSPSSLSASVGDRTVITTCRARSISTYINMWYQKRGKAPKLLIYAASSLQSGVPSRF 60
 QY 61 SGSGGTFTLTITSLNLPEDFASYYCOOSYTTLYTFGSGTLEIKR 106
 DB 61 SGSGGTFTLTITSLNLPEDFATYTCOOSYSTPQFGGTLEIKR 106

RESULT 11
 AAY98245 ID AAY98245 standard; Protein; 107 AA.
 AC AAY98245;
 XX
 XX 04-JUL-2000 (first entry)
 DT
 DE Anti-gp120 antibody light chain variable region from clone B27.
 XX
 XX Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.
 XX
 OS Homo sapiens.
 XX
 XX AU9948754-A.
 PN
 XX 17-FEB-2000.
 PD
 XX 16-SEP-1999; 99AU-0048754.
 PF
 XX 16-SEP-1999; 99AU-0048754.
 PR
 XX 16-SEP-1999; 99AU-0048754.
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Burton DR, Barbas CF, Lerner RA;
 DR WPI; 2000-246867/22.
 XX
 PT Human neutralizing monoclonal antibodies to human immunodeficiency
 PT virus (HIV) used for providing passive immunotherapy to HIV are
 PT specific for glycoprotein-120 -
 XX
 XX Example 9; Figure 11; 374pp; English.
 XX
 CC This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody
 CC capable of reducing an HIV infectivity titre in an in vitro virus
 CC infectivity assay by 50% at a concentration of less than 70 ng/ml. The
 CC method for the production of the antibody comprises:
 CC (a) providing a first polynucleotide encoding a heavy chain
 CC immunoglobulin amino acid sequence (which does not comprise the sequence
 CC represented by AAY98206) and a second polynucleotide encoding a light
 CC chain immunoglobulin amino acid sequence;
 CC (b) inserting the first and second polynucleotide sequences into a host
 CC cell;
 CC (c) maintaining the host cell in conditions which allow the amino acid
 CC sequences encoded by the polynucleotides to be expressed in the host
 CC cell; and
 CC (d) isolating the antibody comprising the heavy and light chain
 CC immunoglobulin amino acid sequences from the host cell.
 CC The anti-HIV gp-120 monoclonal antibody is used for providing passive
 CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used
 CC for neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting
 CC HIV in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those

CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the
 CC antibodies associated with monoclonal antibodies of xenogenic or
 CC chimeric derivation.
 XX
 SQ Sequence 107 AA;
 XX

Query Match 87.0%; Score 476; DB 21; Length 107;
 Best Local Similarity 87.7%; Pred. No. 4.1e-26;
 Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARSISTYINMWYQKRGKAPKLLIMSASNLQSGVPSRF 60
 DB 1 ELTQSPSSLSASVGDRTVITTCRARSISTYINMWYQKRGKAPKLLIYAASSLQSGVPSRF 60
 QY 61 SGSGGTFTLTITSLNLPEDFASYYCOOSYTTLYTFGSGTLEIKR 106
 DB 61 SGSGGTFTLTITSLNLPEDFATYTCOOSYSTPQFGGTLEIKR 106

RESULT 12
 AAG93663 ID AAG93663 standard; Protein; 107 AA.
 AC AAG93663;
 XX
 XX 14-SEP-2001 (first entry)
 DT
 DE Human anti-Rh(D) antibody clone SH49 protein sequence.
 XX
 XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.
 KW
 XX
 OS Homo sapiens.
 XX
 XX US6255455-B1.
 PN
 XX 03-JUL-2001.
 PD
 XX 29-JAN-1999; 99US-0240274.
 PF
 XX 11-OCT-1996; 96US-0028550.
 PR 10-APR-1998; 98US-0081380.
 PR 27-JUN-1997; 97US-0884045.
 XX
 PA (UTPE-) UNIV PENNSYLVANIA.
 PI
 PI Siegel DL;
 DR WPI; 2001-388931/41.
 DR N-PBDB; AAH68720.
 XX
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine -
 XX
 PS Claim 1; Column 69; 162pp; English.
 XX
 CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (8) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.

XX Sequence 107 AA;
 SQ Query Match 86.8%; Score 475; DB 22; Length 107;
 Best Local Similarity 85.8%; Pred. No. 4.8e-26;
 Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTGSPSSLSASVGDVITTCRARSISITLYLWYQKPGKAPKLLIWSANLQSGVPSRF 60
 DB 2 ELTGSPSSLSASVGDVITTCRARSISITLYLWYQKPGKAPKLLIWSANLQSGVPSRF 61
 QY 61 SSGSGTTEFTLTISNLQFEDPASYYCOQSYTTLTYFGSGTKLEIKR 106
 DB 62 SSGSGTDEFTLTITSSLOPEDFATYYCOQSYSTPWTGQGTKEIKR 107

RESULT 13
 AAG93664
 ID AAG93664 standard; Protein; 107 AA.
 AC AAG93664;
 DT 14-SEP-2001 (first entry)
 DE Human anti-Rh(D) antibody clone SH50 protein sequence.
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KM red blood cell; Rh phenotype; diagnosis; therapeutic.
 OS Homo sapiens.
 XX US6255455-B1.
 PN 03-JUL-2001.
 PD 29-JAN-1999; 99US-0240274.
 PF 11-OCT-1996; 96US-0028550.
 PR 10-APR-1998; 98US-0081380.
 PR 27-JUN-1997; 97US-0884045.
 XX (TYPE-) UNIV PENNSYLVANIA.
 PA Siegel DL;
 PI WPI; 2001-388931/41.
 DR N-PSDB; AAH68721.
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine -
 PS Claim 1; Column 69; 162pp; English.
 CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (1) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (1) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (1) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH6615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.
 XX Sequence 107 AA;
 SQ Query Match 86.8%; Score 475; DB 22; Length 107;
 Best Local Similarity 85.8%; Pred. No. 4.8e-26;
 Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTGSPSSLSASVGDVITTCRARSISITLYLWYQKPGKAPKLLIWSANLQSGVPSRF 60

DB 2 ELTGSPSSLSASVGDVITTCRARSISITLYLWYQKPGKAPKLLIWSANLQSGVPSRF 61
 QY 61 SSGSGTTEFTLTISNLQFEDPASYYCOQSYTTLTYFGSGTKLEIKR 106
 DB 62 SSGSGTDEFTLTITSSLOPEDFATYYCOQSYSTPWTGQGTKEIKR 107

RESULT 14
 AAG93667
 ID AAG93667 standard; Protein; 107 AA.
 AC AAG93667;
 DT 14-SEP-2001 (first entry)
 DE Human anti-Rh(D) antibody clone SH54 protein sequence.
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KM red blood cell; Rh phenotype; diagnosis; therapeutic.
 OS Homo sapiens.
 XX US6255455-B1.
 PN 03-JUL-2001.
 PD 29-JAN-1999; 99US-0240274.
 PF 11-OCT-1996; 96US-0028550.
 PR 10-APR-1998; 98US-0081380.
 PR 27-JUN-1997; 97US-0884045.
 XX (TYPE-) UNIV PENNSYLVANIA.
 PA Siegel DL;
 PI WPI; 2001-388931/41.
 DR N-PSDB; AAH68724.
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine -
 PS Claim 1; Column 70; 162pp; English.
 CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (1) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (1) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (1) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH6615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.
 XX Sequence 107 AA;
 SQ Query Match 86.7%; Score 474; DB 22; Length 107;
 Best Local Similarity 85.8%; Pred. No. 5.6e-26;
 Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTGSPSSLSASVGDVITTCRARSISITLYLWYQKPGKAPKLLIWSANLQSGVPSRF 60
 DB 2 ELTGSPSSLSASVGDVITTCRARSISITLYLWYQKPGKAPKLLIWSANLQSGVPSRF 61
 QY 61 SSGSGTTEFTLTISNLQFEDPASYYCOQSYTTLTYFGSGTKLEIKR 106
 DB 62 SSGSGTDEFTLTITSSLOPEDFATYYCOQSYSTPWTGQGTKEIKR 107


```

RESULT 15
AAG93589
ID AAG93589 standard; Protein; 108 AA.
XX
AC AAG93589;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) chain I01 protein sequence.
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
OS Homo sapiens.
XX
PN US6255455-B1.
XX
PD 03-JUL-2001.
XX
PF 29-JAN-1999; 99US-0240274.
XX
PR 11-OCT-1996; 96US-0028550.
PR 10-APR-1998; 98US-0081380.
PR 27-JUN-1997; 97US-0884045.
XX
PA (TYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR MPI; 2001-388931/41.
DR N-PSDB; AAH68646.
XX
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine -
XX
PS Claim 1; Column 43; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification
CC of the present invention.
XX
SQ Sequence 108 AA;

Query Match 86.6%; Score 473.5; DB 22; Length 108;
Best Local Similarity 87.9%; Pred No. 6,1e-26;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTGSPSSISASVGRVITTCRARSISTYLNWYQOKPGKAPKLLIWSASNLQGVPSRF 60
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DB 2 ELTGSPSSISASVGRVITTCRARSISTYLNWYQOKPGKAPKLLIWSASNLQGVPSRF 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGGTETFTLTISNLQFEDFASYYCQOSYTT-LTFPGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 62 SSGSGGTETFTLTISNLQFEDFASYYCQOSYTPPYTFGGTKLEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-10-027-725A-11

Perfect score: 547
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Scoring table:
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Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/FCI_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	547	100.0	106	US-10-027-725A-11	Sequence 11, Appl
2	484	88.5	107	US-10-016-986-104	Sequence 104, App
3	483	88.3	107	US-09-848-798-33	Sequence 33, Appl
4	480	87.8	107	US-09-848-798-156	Sequence 156, App
5	476	87.0	107	US-10-016-986-105	Sequence 105, App
6	475	86.8	107	US-09-848-798-175	Sequence 175, App
7	475	86.8	107	US-09-848-798-176	Sequence 176, App
8	474	86.7	107	US-09-848-798-179	Sequence 179, App
9	473.5	86.6	108	US-09-848-798-32	Sequence 32, Appl
10	473.5	86.6	108	US-09-848-798-43	Sequence 43, Appl
11	473	86.5	107	US-09-848-798-37	Sequence 37, Appl
12	473	86.5	111	US-10-203-754A-57	Sequence 57, Appl
13	472.5	86.4	108	US-09-848-798-167	Sequence 167, App
14	472	86.3	107	US-09-848-798-38	Sequence 38, Appl
15	472	86.3	107	US-09-848-798-39	Sequence 39, Appl

16	472	86.3	107	US-09-848-798-162	Sequence 162, App
17	471	86.1	107	US-09-848-798-158	Sequence 158, App
18	469	85.7	107	US-09-848-798-44	Sequence 44, Appl
19	468	85.6	111	US-10-203-754A-56	Sequence 56, Appl
20	467	85.4	240	US-09-192-854-2	Sequence 2, Appl1
21	467	85.4	240	US-09-968-561A-2	Sequence 2, Appl1
22	467	85.4	240	US-09-968-744A-2	Sequence 2, Appl1
23	466	85.2	107	US-09-791-153A-67	Sequence 67, Appl
24	465	85.0	107	US-10-309-762-89	Sequence 89, Appl
25	464.5	84.9	108	US-09-848-798-163	Sequence 163, App
26	463	84.6	104	US-10-016-986-106	Sequence 106, App
27	463	84.6	107	US-10-309-762-88	Sequence 88, Appl
28	462	84.5	127	US-10-309-762-101	Sequence 101, App
29	460	84.1	105	US-10-027-725A-10	Sequence 10, Appl
30	459	83.9	107	US-09-848-798-168	Sequence 168, App
31	458	83.7	106	US-10-377-121-5	Sequence 5, Appl1
32	457	83.5	107	US-09-848-798-36	Sequence 36, Appl
33	457	83.5	214	US-10-153-382-19	Sequence 19, Appl
34	456.5	83.5	108	US-09-848-798-41	Sequence 41, Appl
35	456.5	83.5	108	US-10-016-986-109	Sequence 109, App
36	456	83.4	105	US-10-309-762-155	Sequence 155, App
37	456	83.4	107	US-09-848-798-173	Sequence 173, App
38	456	83.4	107	US-10-309-762-67	Sequence 67, Appl
39	456	83.4	107	US-10-309-762-68	Sequence 68, Appl
40	454	83.0	107	US-09-848-798-40	Sequence 40, Appl
41	454	83.0	107	US-10-016-986-103	Sequence 103, App
42	453.5	82.9	114	US-10-364-743-54	Sequence 54, Appl
43	453	82.8	107	US-10-309-762-66	Sequence 66, Appl
44	453	82.8	107	US-10-309-762-69	Sequence 69, Appl
45	453	82.8	108	US-10-025-687-8	Sequence 8, Appl1

ALIGNMENTS

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RESULT 1
US-10-027-725A-11
; Sequence 11, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Fliker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-11

Query Match      100.0%; Score 547; DB 15; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.2e-42;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 ELTQSPSSLSASVGDRTVITGRAROSISTYTNWYQOKGKAPKLIMASNLQGVPRF 60
      |||
QY      61 SGSGSGTEFTLTISNLOPEDFASYCCQGSYTTLYTFSGSKLEIKR 106
      |||
DB      61 SGSGSGTEFTLTISNLOPEDFASYCCQGSYTTLYTFSGSKLEIKR 106
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RESULT 2
US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
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; APPLICANT: Barton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Ierner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
; US-10-016-986-104

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Query Match      484;   Score 88.5%;   Length 107;
Best Local Similarity 88.7%;   Pred. No. 1.6e-36;
Matches 94;   Conservative 8;   Mismatches 4;   Indels 0;   Gaps 0;

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[illegible]

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Qy      61 SSGSGTEFTLTISNLQPEDFASYCCQSQSYTLTYTFGSGTKLEIKR 106
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Db      61 SSGSGCDFTLTISSLPEDFATYYCCQSQSYSPYTFGQGTKLEIKR 106

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RESULT 3
US-09-848-798-33

Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
 FILE REFERENCE: 09596-42U2
 CURRENT APPLICATION NUMBER: US/09/848,798

CURRENT FILING DATE: 2001-03-04
 PRIOR APPLICATION NUMBER: 09/240,274
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550

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; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-11
;
; NUMBER OF SEQ ID NOS: 224
;
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33

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; LENGTH: 10/
; TYPE: PRT
; ORGANISM: Homo sapiens
FEATURE:

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; OTHER INFORMATION: ANCI-KN(D) CHAIN 102
US-09-848-798-33
Query Match      88.3%; Score 483; DB 11; Length 107;

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Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 1
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Db 2 ELQPSSTLSASVGRVITTCRASQSSISSYLNMWQQKPGKAPKLIIYAASSLQSGVPSRF 61

QY 61 SSGSGSGTEFTLLISNIQFEDFASYYCQDSYTLTYFGSGTKLEIKR 106

Db 62 SSGSGSGTDFLLTILSSIQPEDFATYYCQDSYSTLTMTFGQGTKEIKR 107

RESULT 4
US-09-848-798-156
Source: 156 Application no/09848798

Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald J.
TITLE OF INVENTION: PH/D1 BINDING PROMOTING AND MACROPHAGALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
 FILE REFERENCE: 09536-42U2
 CURRENT APPLICATION NUMBER: US/09/848,798
 PUBLICATION NUMBER: 2003/05/04

PRIOR APPLICATION NUMBER: 09/240,274
 PRIOR FILING DATE: 1999-01-29
 PRIOR APPLICATION NUMBER: 60/028,550

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;-----
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156

```

```

LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
```

US-09-848-798-156

CHILD AND CUSTODIAN: BULL, MARCO / WATTSBOY, CARMEN ERNE

Query Match 87.8%; Score 480; DB 11; Length 107;

By	1	ELTSPSSLSASVGDRTTITRRARQISITLYLNWYQKRGKAPKLLTWSASNLQSGVPSRF	60
		Best local similarity	87.78; Freq. NO. 2.0E-20
Matches	93;	Conservative	9; Mismatches 4; Indels 0; Gaps

Db 2 ELTQSPSSLSASVGDRTVITCRASQGISLYLNMVQQRKAKPULLIYAASSLRGVSRRF 61

Db 62 SGSSGTDFTLTISSIQPEDATYYCQSYSPYTFGGTKLEIKR 107

RESULT 5
US-10-016-986-105
; Sequence 105, Application US/10016986
; Publication No. US20030187247A1

```

; GENERAL INFORMATION:
;
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Ierner, Richard A

```

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;
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
;
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
;
; FILE REFERENCE: 313.2CON1
;
; CITIZENSHIP ADDICTION NUMBER: IIS/10/016 986
;

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: CURRENT FILING DATE: 2001-12-12
: PRIOR APPLICATION NUMBER: US 09/149,998
: PRIOR FILING DATE: 1998-09-08
: PRIOR APPLICATION NUMBER: US 08/899,575

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;; PRIOR FILING DATE: 1997-07-24
;; PRIOR APPLICATION NUMBER: US 08/276,852
;; PRIOR FILING DATE: 1994-07-18
;; PRIOR APPLICATION NUMBER: US 08/178,303

PRIOR FILING DATE: 1994-01-06
PRIOR APPLICATION NUMBER: PCT/US93/09328
PRIOR FILING DATE: 1993-09-30
PCT FILING DATE: 1994-05-14
PCT APPLICATION NUMBER: 1994/02541

```

; PRIOR FILING DATE: 1992-09-30
;
; NUMBER OF SEQ ID NOS: 176
;
; SOFTWARE: FastSeq for Windows, Version 4.0
;

```

SEQ ID NO 105
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized
US-10-016-986-105

Query Match 87.0%; Score 476; DB 12; Length 107;
Best Local Similarity 87.7%; Pred. No. 8.3e-36;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Cy 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKRGKAPKLLIWSASNLQSGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKRGKAPKLLIYAASLSQSGVPSRF 60
Cy 61 SSGSGTEFTLTISNLQEPEDPASYCCOQSYTTLVTFPGSGTKLEIKR 106
Db 61 SSGSGGTDFTLTISLQPEDPASYCCOQSYSTPOTFGGTKEIKR 106

RESULT 6

US-09-848-798-175
Sequence 175, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 175
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

Query Match 86.8%; Score 475; DB 11; Length 107;
Best Local Similarity 85.8%; Pred. No. 1e-35; Indels 0; Gaps 0;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Cy 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKRGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKRGKAPKLLIYAASLSQSGVPSRF 61
Cy 61 SSGSGTEFTLTISNLQEPEDPASYCCOQSYTTLVTFPGSGTKLEIKR 106
Db 62 SSGSGGTDFTLTISLQPEDPASYCCOQSYSTPOTFGGTKEIKR 107

RESULT 7

US-09-848-798-176
Sequence 176, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550

PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 176
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-848-798-176

Query Match 86.8%; Score 475; DB 11; Length 107;
Best Local Similarity 85.8%; Pred. No. 1e-35; Indels 0; Gaps 0;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Cy 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKRGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKRGKAPKLLIYAASLSQSGVPSRF 61
Cy 61 SSGSGTEFTLTISNLQEPEDPASYCCOQSYTTLVTFPGSGTKLEIKR 106
Db 62 SSGSGGTDFTLTISLQPEDPASYCCOQSYSTPOTFGGTKEIKR 107

RESULT 8

US-09-848-798-179
Sequence 179, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 179
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179

Query Match 86.7%; Score 474; DB 11; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.3e-35; Indels 0; Gaps 0;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

Cy 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKRGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITCRAROSISTYLNWYQOKRGKAPKLLIYAASLSQSGVPSRF 61
Cy 61 SSGSGTEFTLTISNLQEPEDPASYCCOQSYTTLVTFPGSGTKLEIKR 106
Db 62 SSGSGGTDFTLTISLQPEDPASYCCOQSYSTPOTFGGTKEIKR 107

RESULT 9

US-09-848-798-32
Sequence 32, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04

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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-848-798-32

Query Match      86.6%; Score 473.5; DB 11; Length 108;
Best Local Similarity 87.9%; Pred. No. 1.4e-35;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

1 ELTQSPSSLSASVGDRTTTCARQGISSTYLMWYQKPGKAPKLLIWSASNLQSGVPSRF 60
2 ELTQSPSSLSASVGDRTTTCARQGISSTYLMWYQKPGKAPKLLIYAASNLQSGVPSRF 61
QY 61 SSGSGSTEFTLTISNLQFEDFASYCCOQSYTT-LYTFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SSGSGSTDFTLTISLQPEDFATYCCOQSYSTPPTFGGQTKLEIKR 108

RESULT 10
US-09-848-798-43
; Sequence 43, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-848-798-43

Query Match      86.6%; Score 473.5; DB 11; Length 108;
Best Local Similarity 87.9%; Pred. No. 1.4e-35;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

1 ELTQSPSSLSASVGDRTTTCARQGISSTYLMWYQKPGKAPKLLIWSASNLQSGVPSRF 60
2 ELTQSPSSLSASVGDRTTTCARQGISSTYLMWYQKPGKAPKLLIYAASNLQSGVPSRF 61
QY 61 SSGSGSTEFTLTISNLQFEDFASYCCOQSYTT-LYTFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SSGSGSTDFTLTISLQPEDFATYCCOQSYSTPPTFGGQTKLEIKR 108

RESULT 11
US-09-848-798-37
; Sequence 37, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I06
US-09-848-798-37

Query Match      86.5%; Score 473; DB 11; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.6e-35;
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

1 ELTQSPSSLSASVGDRTTTCARQGISSTYLMWYQKPGKAPKLLIWSASNLQSGVPSRF 60
2 ELTQSPSSLSASVGDRTTTCARQGISSTYLMWYQKPGKAPKLLIYAASNLQSGVPSRF 61
QY 61 SSGSGSTEFTLTISNLQFEDFASYCCOQSYTT-LYTFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SSGSGSTDFTLTISLQPEDFATYCCOQSYSTPPTFGGQTKLEIKR 108
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; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I06
US-09-848-798-37

Query Match      86.5%; Score 473; DB 11; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.6e-35;
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

1 ELTQSPSSLSASVGDRTTTCARQGISSTYLMWYQKPGKAPKLLIWSASNLQSGVPSRF 60
2 ELTQSPSSLSASVGDRTTTCARQGISSTYLMWYQKPGKAPKLLIYAASNLQSGVPSRF 61
QY 61 SSGSGSTEFTLTISNLQFEDFASYCCOQSYTT-LYTFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SSGSGSTDFTLTISLQPEDFATYCCOQSYSTPPTFGGQTKLEIKR 108

RESULT 12
US-10-203-754A-57
; Sequence 57, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
; APPLICANT: SEKI, Makoto
; APPLICANT: MATSURA, Yoshiharu
; APPLICANT: SHIBUI, Tatsuro
; APPLICANT: YOTSUMOTO, Yoshihisa
; APPLICANT: MIYAMURA, Tatsuo
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-203-754A-57

Query Match      86.5%; Score 473; DB 12; Length 111;
Best Local Similarity 86.7%; Pred. No. 1.6e-35;
Matches 91; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

2 LTQSPSSLSASVGDRTTTCARQGISSTYLMWYQKPGKAPKLLIWSASNLQSGVPSRF 61
4 MTQSPSSLSASVGDRTTTCARQGISSTYLMWYQKPGKAPKLLIYAASNLQSGVPSRF 63
QY 62 SSGSGSTEFTLTISNLQFEDFASYCCOQSYTT-LYTFGSGTKLEIKR 106
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 SSGSGSTDFTLTISLQPEDFATYCCOQSYTPTFGGQTKLEIKR 108

RESULT 13
US-09-848-798-167
; Sequence 167, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
```

```
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 167
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH34
US-09-848-798-167
```

```
Query Match      86.3%; Score 472; DB 11; Length 108;
Best Local Similarity 87.9%; Pred. No. 1.7e-35;
Matches 94; Conservative 7; Mismatches 5; Indels 1; Gaps 1;
```

```
QY 1 ELTQSPSSLSASVGDVVTTCRAQOSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 60
    |||
DB 2 ELTQSPSSLSASVGDVVTTCRAQOSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 61
    |||
QY 61 SSGSGCTEFTLTISNLOPEDFASYYCOOSYTT-LYTFGSGTLEIKR 106
    |||
DB 62 SSGSGCTDFTLTISLQPEDFATYYCOOSYSTPRTFGGTVEIKR 108
    |||
```

RESULT 14
US-09-848-798-38

```
Sequence 38, Application US/09848798
Publication No. US20030040605A1
```

```
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 38
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 107
US-09-848-798-38
```

```
Query Match      86.3%; Score 472; DB 11; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.9e-35;
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
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```
QY 1 ELTQSPSSLSASVGDVVTTCRAQOSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 60
    |||
DB 2 ELTQSPSSLSASVGDVVTTCRAQOSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 61
    |||
QY 61 SSGSGCTEFTLTISNLOPEDFASYYCOOSYTTLYTFGSGTLEIKR 106
    |||
DB 62 SSGSGCTDFTLTISLQPEDFATYYCOOSYSTPRTFGGTVEIKR 107
    |||
```

RESULT 15
US-09-848-798-39

```
Sequence 39, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 108
US-09-848-798-39
```

```
Query Match      86.3%; Score 472; DB 11; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.9e-35;
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSLSASVGDVVTTCRAQOSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 60
    |||
DB 2 ELTQSPSSLSASVGDVVTTCRAQOSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 61
    |||
QY 61 SSGSGCTEFTLTISNLOPEDFASYYCOOSYTTLYTFGSGTLEIKR 106
    |||
DB 62 SSGSGCTDFTLTISLQPEDFATYYCOOSYSTPRTFGGTVEIKR 107
    |||
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Search completed: February 10, 2004, 19:03:04
Job time : 25.4121 secs

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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:32:44 ; Search time 10.9212 Seconds
(without alignments)
410.664 Million cell updates/sec

Title: US-10-027-725A-11

Perfect score: 547
Sequence: 1 ELNQPSPSLASVGDRTVIT.....QQSYTTLVTFSGTKLEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pap:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pap:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pap:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pap:*
5: /cgn2_6/ptodata/1/1aa/PCIVS.COMB.pap:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	484	88.5	107	1 US-08-276-852-104	Sequence 104, App
2	484	88.5	107	1 US-08-899-575-104	Sequence 104, App
3	484	88.5	107	1 US-08-899-575-104	Sequence 104, App
4	484	88.5	107	5 PCT-US95-08743-104	Sequence 104, App
5	483	88.3	107	3 US-09-240-274-33	Sequence 33, App1
6	480	87.8	107	3 US-09-240-274-156	Sequence 156, App
7	476	87.0	107	1 US-08-276-852-105	Sequence 105, App
8	476	87.0	107	1 US-08-899-575-105	Sequence 105, App
9	476	87.0	107	1 US-08-899-575-105	Sequence 105, App
10	476	87.0	107	5 PCT-US95-08743-105	Sequence 105, App
11	475	86.8	107	3 US-09-240-274-175	Sequence 175, App
12	475	86.8	107	3 US-09-240-274-176	Sequence 176, App
13	474	86.7	107	3 US-09-240-274-179	Sequence 179, App
14	473.5	86.6	108	3 US-09-240-274-32	Sequence 32, App1
15	473.5	86.6	108	3 US-09-240-274-43	Sequence 43, App1
16	473	86.5	107	3 US-09-240-274-37	Sequence 37, App1
17	472.5	86.4	108	3 US-09-240-274-167	Sequence 167, App
18	472	86.3	107	3 US-09-240-274-38	Sequence 38, App1
19	472	86.3	107	3 US-09-240-274-39	Sequence 39, App1
20	472	86.3	107	3 US-09-240-274-162	Sequence 162, App
21	471	86.1	107	3 US-09-240-274-158	Sequence 158, App
22	469	85.7	107	3 US-09-240-274-44	Sequence 44, App1
23	468	85.6	108	3 US-08-379-057-29	Sequence 29, App1
24	464.5	84.9	108	3 US-09-240-274-163	Sequence 163, App
25	463	84.6	104	1 US-08-276-852-106	Sequence 106, App
26	463	84.6	104	1 US-08-899-575-106	Sequence 106, App
27	463	84.6	104	1 US-08-899-575-106	Sequence 106, App

28	463	84.6	104	5 PCT-US95-08743-106	Sequence 106, App
29	461	84.3	108	4 US-09-025-769B-14	Sequence 14, App1
30	459	83.9	107	1 US-08-300-386A-66	Sequence 66, App1
31	459	83.9	107	3 US-08-931-645-66	Sequence 66, App1
32	459	83.9	107	3 US-09-240-274-168	Sequence 168, App1
33	459	83.9	107	5 PCT-US95-11235-66	Sequence 66, App1
34	457	83.5	107	3 US-09-240-274-36	Sequence 36, App1
35	457	83.5	109	3 US-09-157-370-3	Sequence 3, App1
36	456.5	83.5	108	1 US-08-276-852-109	Sequence 109, App
37	456.5	83.5	108	1 US-08-899-575-109	Sequence 109, App
38	456.5	83.5	108	1 US-08-899-575-109	Sequence 109, App
39	456.5	83.5	108	3 US-09-240-274-109	Sequence 41, App1
40	456.5	83.5	108	5 PCT-US95-08743-109	Sequence 109, App
41	456	83.4	107	3 US-09-240-274-173	Sequence 173, App
42	454	83.0	107	1 US-08-276-852-103	Sequence 103, App
43	454	83.0	107	1 US-08-899-575-103	Sequence 103, App
44	454	83.0	107	1 US-08-899-575-103	Sequence 103, App
45	454	83.0	107	3 US-09-240-274-40	Sequence 40, App1

ALIGNMENTS

RESULT 1
US-08-276-852-104
; Sequence 104, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-852-104

RESULT 4
PCT-US95-08743-104
; Sequence 104, Application PC/TUS9508743

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; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-104

Query Match      88.5%; Score 484; DB 5; Length 107;
Best Local Similarity 88.7%; Pred. No. 1.1e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCARQSIQSYLNWYQOKRGKAPKLIWSASNLQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITTCARQSIQSYLNWYQOKRGKAPKLIWSASNLQGVPSRF 60
Qy 61 SSGSGGTEFTLTISNLQFEDFASYYCCQSYTTLYTFPGSGTKLEIKR 106
Db 61 SSGSGGTEFTLTISNLQFEDFASYYCCQSYTTLYTFPGSGTKLEIKR 106
Db 62 SSGSGGTEFTLTISNLQFEDFASYYCCQSYTTLYTFPGSGTKLEIKR 106

RESULT 5
US-09-240-274-33
; Sequence 33, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
; US-09-240-274-33

Query Match      88.3%; Score 483; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-36;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCARQSIQSYLNWYQOKRGKAPKLIWSASNLQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCARQSIQSYLNWYQOKRGKAPKLIWSASNLQGVPSRF 61
Qy 61 SSGSGGTEFTLTISNLQFEDFASYYCCQSYTTLYTFPGSGTKLEIKR 106
Db 62 SSGSGGTEFTLTISNLQFEDFASYYCCQSYTTLYTFPGSGTKLEIKR 107
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RESULT 6
US-09-240-274-156
; Sequence 156, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
; US-09-240-274-156

Query Match      87.8%; Score 480; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.4e-36;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITTCARQSIQSYLNWYQOKRGKAPKLIWSASNLQGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCARQSIQSYLNWYQOKRGKAPKLIWSASNLQGVPSRF 61
Qy 61 SSGSGGTEFTLTISNLQFEDFASYYCCQSYTTLYTFPGSGTKLEIKR 106
Db 62 SSGSGGTEFTLTISNLQFEDFASYYCCQSYTTLYTFPGSGTKLEIKR 107

RESULT 7
US-08-276-852-105
; Sequence 105, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: Mail Drop 1PC8
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-105

Query Match 87.0%; Score 476; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 5.5e-36;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGVDRVTTCRAPQISITVYLNWYQOKPGKAPKLIWSASNLQGVPSRF 60
DB 1 ELTQSPSSLSASVGVDRVTTCRAPQISITVYLNWYQOKPGKAPKLIWSASNLQGVPSRF 60
QY 61 SSGSGCTEFTLTISNLOFEDFASYCCQSYTTLTYFGSGTKLEIKR 106
DB 61 SSGSGCTDFTLTISLQPEDFATYYCQGSYSTPTQGTGKLEIKR 106

RESULT 8
US-08-899-575-105

Sequence 105, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-105

Query Match 87.0%; Score 476; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 5.5e-36;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGVDRVTTCRAPQISITVYLNWYQOKPGKAPKLIWSASNLQGVPSRF 60
DB 1 ELTQSPSSLSASVGVDRVTTCRAPQISITVYLNWYQOKPGKAPKLIWSASNLQGVPSRF 60
QY 61 SSGSGCTEFTLTISNLOFEDFASYCCQSYTTLTYFGSGTKLEIKR 106
DB 61 SSGSGCTDFTLTISLQPEDFATYYCQGSYSTPTQGTGKLEIKR 106

RESULT 9

US-08-899-575-105
Sequence 105, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-105

Query Match 87.0%; Score 476; DB 1; Length 107;
 Best Local Similarity 87.7%; Pred. No. 5.5e-36;
 Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGDVGVTTTCRAOSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 60
 DB 1 ELTOSPSLSASVGDVGVTTTCRAOSISTYLNWYQOKPKAKPLIYASLSQSGVPSRF 60

QY 61 SSGSGTEFTLTISNLQFEDPASYYCOOSYTTLYTFGSGTKLEIKR 106
 DB 61 SSGSGTDFTLTISLQPEDFATYYCOOSYSTPTFGGTKEIKR 106

RESULT 10

PCT-US95-08743-105
 ; Sequence 105, Application PC/TUS9508743
 ; GENERAL INFORMATION:

APPLICANT:
 TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 NUMBER OF SEQUENCES: 170
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/08743
 FILING DATE: 11-JUL-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/276,852
 FILING DATE: 18-JUL-1994
 INFORMATION FOR SEQ ID NO: 105:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-08743-105

Query Match 87.0%; Score 476; DB 5; Length 107;
 Best Local Similarity 87.7%; Pred. No. 5.5e-36;
 Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGDVGVTTTCRAOSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 60
 DB 1 ELTOSPSLSASVGDVGVTTTCRAOSISTYLNWYQOKPKAKPLIYASLSQSGVPSRF 60

QY 61 SSGSGTEFTLTISNLQFEDPASYYCOOSYTTLYTFGSGTKLEIKR 106
 DB 61 SSGSGTDFTLTISLQPEDFATYYCOOSYSTPTFGGTKEIKR 106

RESULT 11

US-09-240-274-175
 ; Sequence 175, Application US/09240274
 ; Patent No. 6255455
 ; GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.
 TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
 TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
 FILE REFERENCE: 09596-4202
 CURRENT APPLICATION NUMBER: US/09/240,274
 CURRENT FILING DATE: 1999-01-29
 EARLIER APPLICATION NUMBER: 60/081,380
 EARLIER FILING DATE: 1998-04-10
 EARLIER APPLICATION NUMBER: 60/028,550
 EARLIER FILING DATE: 1996-10-11
 NUMBER OF SEQ ID NOS: 224
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 175
 LENGTH: 107

TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: anti-Rh(D) antibody clone SH49
 US-09-240-274-175

Query Match 86.8%; Score 475; DB 3; Length 107;
 Best Local Similarity 85.8%; Pred. No. 6.8e-36;
 Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGDVGVTTTCRAOSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 60
 DB 2 ELTOSPSLSASVGDVGVTTTCRAOSISTYLNWYQOKPKAKPLIYASLSQSGVPSRF 61

QY 61 SSGSGTEFTLTISNLQFEDPASYYCOOSYTTLYTFGSGTKLEIKR 106
 DB 62 SSGSGTDFTLTISLQPEDFATYYCOOSYSTPTFGGTKEIKR 107

RESULT 12

US-09-240-274-176
 ; Sequence 176, Application US/09240274
 ; Patent No. 6255455
 ; GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.
 TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
 TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
 FILE REFERENCE: 09596-4202
 CURRENT APPLICATION NUMBER: US/09/240,274
 CURRENT FILING DATE: 1999-01-29
 EARLIER APPLICATION NUMBER: 60/081,380
 EARLIER FILING DATE: 1998-04-10
 EARLIER APPLICATION NUMBER: 60/028,550
 EARLIER FILING DATE: 1996-10-11
 NUMBER OF SEQ ID NOS: 224
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 176
 LENGTH: 107
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:

OTHER INFORMATION: anti-Rh(D) antibody clone SH50
 US-09-240-274-176

Query Match 86.8%; Score 475; DB 3; Length 107;
 Best Local Similarity 85.8%; Pred. No. 6.8e-36;
 Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGDVGVTTTCRAOSISTYLNWYQOKPKAKPLIWSASNLQSGVPSRF 60
 DB 2 ELTOSPSLSASVGDVGVTTTCRAOSISTYLNWYQOKPKAKPLIYASLSQSGVPSRF 61

QY 61 SSGSGTEFTLTISNLQFEDPASYYCOOSYTTLYTFGSGTKLEIKR 106
 DB 62 SSGSGTDFTLTISLQPEDFATYYCOOSYSTPTFGGTKEIKR 107

RESULT 13

US-09-240-274-179
 ; Sequence 179, Application US/09240274
 ; Patent No. 6255455
 ; GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.
 TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
 TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
 FILE REFERENCE: 09596-4202
 CURRENT APPLICATION NUMBER: US/09/240,274
 CURRENT FILING DATE: 1999-01-29
 EARLIER APPLICATION NUMBER: 60/081,380
 EARLIER FILING DATE: 1998-04-10
 EARLIER APPLICATION NUMBER: 60/028,550
 EARLIER FILING DATE: 1996-10-11
 NUMBER OF SEQ ID NOS: 224

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; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-179

Query Match      86.7%; Score 474; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 8.3e-36;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTITTCRAROSISTYLMWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTITTCRAROSISTYLMWYQOKPGKAPKLLIYAASSLQSGVPSRF 61

QY 61 SSGSGGTFTLTISNLQFEDFASYCCOOSYTT-LYFGSGTKLEIKR 106
DB 62 SSGSGGTFTLTISNLQFEDFASYCCOOSYSTPTPTFGGTKLEIKR 107

RESULT 14
US-09-240-274-32
; Sequence 32, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-240-274-32

Query Match      86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 9.3e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTITTCRAROSISTYLMWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTITTCRAROSISTYLMWYQOKPGKAPKLLIYAASSLQSGVPSRF 61

QY 61 SSGSGGTFTLTISNLQFEDFASYCCOOSYTT-LYFGSGTKLEIKR 106
DB 62 SSGSGGTFTLTISNLQFEDFASYCCOOSYSTPTPTFGGTKLEIKR 108

RESULT 15
US-09-240-274-43
; Sequence 43, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
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; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-240-274-43

Query Match      86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 9.3e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTITTCRAROSISTYLMWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTITTCRAROSISTYLMWYQOKPGKAPKLLIYAASSLQSGVPSRF 61

QY 61 SSGSGGTFTLTISNLQFEDFASYCCOOSYTT-LYFGSGTKLEIKR 106
DB 62 SSGSGGTFTLTISNLQFEDFASYCCOOSYSTPTPTFGGTKLEIKR 108
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Search completed: February 10, 2004, 18:42:09
Job time : 11.9212 secs

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OM protein - protein search, using sw model

Run on: February 10, 2004, 18:26:58 ; Search time 10.9212 Seconds
(without alignments)
933.402 Million cell updates/sec

Title: US-10-027-725A-12

Sequence: 1 ELTQSPSSVSASVGDRTVIT.....QQANSFPTFGQTKVEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*

1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	84.2	117	2	S46376 Ig kappa chain V-J
2	462	84.2	125	2	S40316 Ig kappa chain - h
3	459	83.6	125	2	S40333 Ig kappa chain V-J
4	455	82.9	125	2	S40349 Ig kappa chain V-J
5	454.5	82.8	130	2	S40336 Ig kappa chain V-J
6	454	82.7	130	2	S40368 Ig kappa chain - h
7	451	82.1	128	2	S46372 Ig kappa chain var
8	451	82.1	131	2	S40352 Ig kappa chain V-J
9	450	82.0	105	2	S36266 Ig kappa chain V
10	447	81.4	127	2	S40367 Ig kappa chain V-J
11	446	81.2	108	2	S18674 Ig kappa chain V r
12	446	81.2	132	2	S38646 Ig kappa chain V r
13	445	81.1	137	2	S46371 Ig kappa chain V-J
14	444	80.9	123	2	S40331 Ig kappa chain - h
15	444	80.9	132	2	S40334 Ig kappa chain - h
16	443	80.7	108	2	B48047 Ig kappa chain V r
17	441	80.3	108	2	S47182 Ig kappa chain - h
18	441	80.3	109	2	S31998 Ig kappa chain - h
19	441	80.3	124	2	S40318 Ig kappa chain V r
20	439.5	80.1	108	2	S30521 Ig kappa chain V r
21	439	80.0	129	2	S40369 Ig kappa chain - h
22	437	79.6	107	2	S36264 Ig kappa chain V
23	435.5	79.3	108	2	S34007 Ig kappa chain V r
24	435	79.2	108	1	K1HUBN Ig kappa chain V-I
25	434.5	79.1	107	2	S36275 Ig kappa chain V
26	434	79.1	108	1	K1HUBS Ig kappa chain V-I
27	434	78.9	117	2	S21527 Ig kappa chain V r
28	433	78.7	108	2	S21527 Ig kappa chain V r
29	432	78.7	108	2	S36283 Ig lambda chain V

30	431.5	78.6	107	2	S47183 Ig kappa chain - h
31	431	78.5	107	2	S36262 Ig lambda chain V
32	428	78.0	107	2	S36269 Ig lambda chain V
33	427	77.8	109	2	S31981 Ig kappa chain - h
34	426.5	77.7	107	1	K1HUBR Ig kappa chain V-I
35	426	77.6	108	2	S36277 Ig kappa chain V
36	426	77.6	109	2	S31979 Ig lambda chain - h
37	426	77.6	110	2	PN0535 Ig kappa chain V r
38	426	77.6	122	2	S40370 Ig kappa chain - h
39	426	77.6	141	2	A49134 Ig kappa chain V-I
40	424	77.2	107	2	I69017 anti-HIV1 envelope
41	424	77.2	108	1	K1HUBE Ig kappa chain V-I
42	424	77.2	129	1	K1HUKK Ig kappa chain pre
43	423	77.0	108	1	K1HUBU Ig kappa chain V-I
44	423	77.0	108	1	K1HUBS Ig kappa chain V-I
45	423	77.0	126	2	S40335 Ig kappa chain V-J

ALIGNMENTS

RESULT 1

S46376
Ig kappa chain V-J region (T13-14) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence #revision 01-Sep-1995 #text_change 21-Jan-2000

C:Accession: S46376; S38649

R:Bensimon, C.; Chastagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(ch1) gene recombination

A:Reference number: S46369; MUID:94313975; PMID:8039491

A:Accession: S46376

A:Molecule type: mRNA

A:Residues: 1-117 <BEN>

A:Cross-references: EMBL:Z27177; NID:G415969; PIDN:CAA81701.1; PID:G415970

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:25-99/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 462; DB 2; Length 117;
Best Local Similarity 84.9%; Pred. No. 2e-32;
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY	1	ELTQSPSSVSASVGDRTVITTRASQGISWLAAYOHQPKKLLIYASASLOGVPERF	60
DB	12	QMTQSPSSVSASISDRTVITTRASQDISWLAAYQOKKPKLLIYASASLOGVPLRF	71
QY	61	SGSGVTDPSLTISLSLOPEDSATYTCOOANSFPTFGQTKVEIKR	106
DB	72	SGSGSDTFTLTISLSLOPEDPATYTCOOANSFPGFGTIVDIKR	117

RESULT 2

S40316
Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1994 #sequence #revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40316

R:Klein, R.; Jaenichen, R.; Zachau, H. G.

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40316

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLE>

A:Cross-references: EMBL:X72426

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:31-105/Domain: immunoglobulin homology <IMM>

Query Match 84.2%; Score 462; DB 2; Length 125;
Best Local Similarity 85.8%; Pred. No. 2.2e-32;

EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re-
A:Reference number: S46369; MUID:94313975; PMID:8035491
A:Accession: S46372
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <BEN>
A:Cross-references: EMBL:Z27173
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 451; DB 2; Length 128;
Best Local Similarity 83.8%; Pred. No. 1.9e-31;
Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 2 LTQSPSSVSVASVGDRTVITTCRASQGISWLAHYOHQPKAPKLIYASASSLQSGVPSRF 61
Db 24 LTQSPSSVSVASVGDRTVITTCRASQGISWLAHYOHQPKAPKLIYASASSLQSGVPSRF 83
Qy 62 GSGGVTDFSLTISLQFEDSATYCCQANSFPYTFGGCTKVEIKR 106
Db 84 GSGGVTDFSLTISLQFEDSATYCCQANSFPYTFGGCTKVEIKR 128

RESULT 8
S40352
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40352
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40352
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-131 <KLE>
A:Cross-references: EMBL:X72462; NID:q441392; PIDN:CA51130.1; PID:q441393
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 451; DB 2; Length 131;
Best Local Similarity 83.0%; Pred. No. 1.9e-31;
Matches 88; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSVASVGDRTVITTCRASQGISWLAHYOHQPKAPKLIYASASSLQSGVPSRF 60
Db 23 QMTQSPSSVSVASVGDRTVITTCRASQGISWLAHYOHQPKAPKLIYASASSLQSGVPSRF 82
Qy 61 GSGGVTDFSLTISLQFEDSATYCCQANSFPYTFGGCTKVEIKR 106
Db 83 GSGGVTDFSLTISLQFEDSATYCCQANSFPYTFGGCTKVEIKR 128

RESULT 9
S36266
Ig lambda chain V region (clone alpha-TNF-E1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36266
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36265; MUID:93178448; PMID:7679990
A:Accession: S36266
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-105 <GRI>
A:Cross-references: EMBL:Z18840; NID:q33423; PIDN:CAA79292.1; PID:g939916
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 450; DB 2; Length 105;
Best Local Similarity 85.3%; Pred. No. 1.9e-31;
Matches 87; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 2 LTQSPSSVSVASVGDRTVITTCRASQGISWLAHYOHQPKAPKLIYASASSLQSGVPSRF 61
Db 4 LTQSPSSVSVASVGDRTVITTCRASQGISWLAHYOHQPKAPKLIYASASSLQSGVPSRF 63
Qy 62 GSGGVTDFSLTISLQFEDSATYCCQANSFPYTFGGCTKVEIKR 103
Db 64 GSGGVTDFSLTISLQFEDSATYCCQANSFPYTFGGCTKVEIKR 105

RESULT 10
S40367
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40367
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40367
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-127 <KLE>
A:Cross-references: EMBL:X72477
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 447; DB 2; Length 127;
Best Local Similarity 82.1%; Pred. No. 4.1e-31;
Matches 87; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSVASVGDRTVITTCRASQGISWLAHYOHQPKAPKLIYASASSLQSGVPSRF 60
Db 20 QMTQSPSSVSVASVGDRTVITTCRASQGISWLAHYOHQPKAPKLIYASASSLQSGVPSRF 79
Qy 61 GSGGVTDFSLTISLQFEDSATYCCQANSFPYTFGGCTKVEIKR 106
Db 80 GSGGVTDFSLTISLQFEDSATYCCQANSFPYTFGGCTKVEIKR 125

RESULT 11
S19674
Ig kappa chain V region (clone alpha-TEL9) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19674
R:Marks, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.
Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A:Reference number: S19663; MUID:92085276; PMID:11748994
A:Accession: S19674
A:Molecule type: mRNA
A:Residues: 1-108 <MAR>
A:Cross-references: EMBL:X61642; NID:q37860; PIDN:CAA3823.1; PID:g1335386
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 446; DB 2; Length 108;
Best Local Similarity 82.9%; Pred. No. 4.2e-31;
Matches 87; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 2 LTQSPSSVSVASVGDRTVITTCRASQGISWLAHYOHQPKAPKLIYASASSLQSGVPSRF 61
Db 4 LTQSPSSVSVASVGDRTVITTCRASQGISWLAHYOHQPKAPKLIYASASSLQSGVPSRF 63

QY 62 GSGYGTDFSLTISLQPEDSATYCCOANSFPYTFGGTKEIKR 106
 C/Accession: S40331
 Db 64 GSGSGTDFTLTISLQPEDFATYCCOQNSFPLTFGGTKEIKR 108

RESULT 12

338646
 Ig kappa chain V region - human (fragment)

C/Species: Homo sapiens (man)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S38646
 R/Beniston, C.; Chastagner, P.; Zouali, M.
 submitted to the EMBL Data Library, November 1993
 A/Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
 A/Reference number: S38643
 A/Accession: S38646
 A/Status: preliminary
 A/Molecule type: mRNA

A/Residues: 1-113 <BEN>
 A/Cross-references: EMBL:Z27173; NID:g415961; PIDN:CAA81697.1; PID:g415962
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:40-114/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 446; DB 2; Length 132;
 Best Local Similarity 82.9%; Pred. No. 5.1e-31;
 Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPKAKPLLIYSASLSQGVPSRF 61
 Ig kappa chain V-J region (T24-3) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
 C/Accession: S46371; S38645
 R/Beniston, C.; Chastagner, P.; Zouali, M.
 EMBL J. 13, 2951-2962, 1994
 A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination
 A/Reference number: S46369; MUID:94313975; PMID:8039491
 A/Accession: S46371
 A/Molecule type: mRNA
 A/Residues: 1-117 <BEN>
 A/Cross-references: EMBL:Z27172; NID:g415959; PIDN:CAA81696.1; PID:g415960
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:23-97/Domain: immunoglobulin homology <IMM>

RESULT 13

S46371
 Ig kappa chain V-J region (T24-3) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
 C/Accession: S46371; S38645
 R/Beniston, C.; Chastagner, P.; Zouali, M.
 EMBL J. 13, 2951-2962, 1994
 A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination
 A/Reference number: S46369; MUID:94313975; PMID:8039491
 A/Accession: S46371
 A/Molecule type: mRNA
 A/Residues: 1-117 <BEN>
 A/Cross-references: EMBL:Z27172; NID:g415959; PIDN:CAA81696.1; PID:g415960
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:23-97/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 445; DB 2; Length 117;
 Best Local Similarity 78.7%; Pred. No. 5.6e-31;
 Matches 85; Conservative 14; Mismatches 7; Indels 2; Gaps 1;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPKAKPLLIYSASLSQGVPSRF 60
 Ig kappa chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
 C/Accession: S40331
 R/Beniston, C.; Chastagner, P.; Zouali, M.
 EMBL J. 13, 2951-2962, 1994
 A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination
 A/Reference number: S40331; MUID:94080891; PMID:8258341
 A/Accession: S40331
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-123 <KLE>
 A/Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PID:g441351
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:32-106/Domain: immunoglobulin homology <IMM>

QY 61 SSGYGTDFSLTISLQPEDSATYCCOANSF--PYTFGGTKEIKR 106
 Ig kappa chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
 C/Accession: S40331
 R/Beniston, C.; Chastagner, P.; Zouali, M.
 EMBL J. 13, 2951-2962, 1994
 A/Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene recombination
 A/Reference number: S40331; MUID:94080891; PMID:8258341
 A/Accession: S40331
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-123 <KLE>
 A/Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PID:g441351
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:32-106/Domain: immunoglobulin homology <IMM>

RESULT 14

S40331
 Ig kappa chain - human
 C/Species: Homo sapiens (man)

C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40331
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40331
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-123 <KLE>
 A/Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PID:g441351
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 444; DB 2; Length 123;
 Best Local Similarity 83.8%; Pred. No. 7.1e-31;
 Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPKAKPLLIYSASLSQGVPSRF 60
 Ig kappa chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40334
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40334
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-132 <KLE>
 A/Cross-references: EMBL:X72444
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:37-111/Domain: immunoglobulin homology <IMM>

RESULT 15

S40334
 Ig kappa chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40334
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40334
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-132 <KLE>
 A/Cross-references: EMBL:X72444
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 80.9%; Score 444; DB 2; Length 132;
 Best Local Similarity 80.2%; Pred. No. 7.6e-31;
 Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLAHYOHQPKAKPLLIYSASLSQGVPSRF 60
 Ig kappa chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40334
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A/Reference number: S40312; MUID:94080891; PMID:8258341
 A/Accession: S40334
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-132 <KLE>
 A/Cross-references: EMBL:X72444
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F:37-111/Domain: immunoglobulin homology <IMM>

Search completed: February 10, 2004, 18:41:11
 Job time : 11.9212 secs


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ID .KV15 HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region W6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzen H., Yang C., Krusche J.U., Hillebrand N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones protein
RT W6).";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR HSP; P80362; 1MTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B1A4649A60E45 CRC64;

Query Match 79.1%; Score 434; DB 1; Length 108;
Best Local Similarity 80.2%; Pred. No. 3.2e-38;
Matches 85; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTTTCRASQGISWLAHYOHOPGAKPKLLTYSASSLSQGVPSRF 60
DB 3 QMTQSPSSVASVGDRTTTCRASQDISHWLAHYOQKSGAPKLLTYSASSLSQGVPSRF 62
QY 61 SSGSGYGTDFSLTISLQFEDSATYTCQOANSFYPTFGQTKVEIKR 106
DB 63 SSGSGGTDFSLTISLQPEDFATYFCQOANSVPLTFGCGTTVDIKR 108

RESULT 3
KV15 HUMAN STANDARD; PRT; 107 AA.
ID .KV15 HUMAN STANDARD; PRT; 107 AA.
AC P01596;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75075135; PubMed=4216454;
RA Milstein C.P., Deverson E.V.;

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RT "Primary structure of kappa light chain from a human myeloma
RT protein.";
RL Eur. J. Biochem. 49:377-391(1974).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC MARKER.
DR PIR; A01864; K1HWAR.
DR HSP; P80362; 1MTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;

Query Match 77.7%; Score 426.5; DB 1; Length 107;
Best Local Similarity 76.4%; Pred. No. 1.9e-37;
Matches 81; Conservative 15; Mismatches 9; Indels 1; Gaps 1;

QY 1 ELTQSPSSVASVGDRTTTCRASQGISWLAHYOHOPGAKPKLLTYSASSLSQGVPSRF 60
DB 3 QMTQSPSSVASVGDRTTTCRASQDISHWLAHYOQKSGAPKLLTYSASSLSQGVPSRF 62
QY 61 SSGSGYGTDFSLTISLQFEDSATYTCQOANSFYPTFGQTKVEIKR 106
DB 63 SSGSGGTDFSLTISLQPEDFATYFCQOANSVPLTFGCGTTVDIKR 107

RESULT 4
KV15 HUMAN STANDARD; PRT; 108 AA.
ID .KV15 HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region W6A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein W6A) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR; A01876; K1HWME.
DR HSP; P80362; 1MTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.

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FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match
Best Local Similarity 77.2%; Score 424; DB 1; Length 108;
Matches 82; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLMAYOHQPGKAPKLLIYASASSLSQGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITTCRASQGISIRNDLTWYQKRGKAPKLLIYAASSLQGVPSRF 62
QY 61 SGGSGYTDFTLITSLQFEDSATYTCQOANSFPYTFGGQTKVEIKR 106
DB 63 SGGSGGTFTLITSLQFEDPATYTCLOQNSFPMTFGQTKVEIKR 108

RESULT 5
KV1W HUMAN STANDARD; PRT; 129 AA.
ID P04431;
AC 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G.; Combrato G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL lymphoid cell lines are closely related.";
CC Nucleic Acids Res. 12:6995-7006 (1984).
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
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CC EMBL, X00965, CA25477.1; ALT_TERM.
DR PIR; A01883; KIHUWK.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129 129

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SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2E9 CRC64;

Query Match
Best Local Similarity 77.2%; Score 424; DB 1; Length 129;
Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLMAYOHQPGKAPKLLIYASASSLSQGVPSRF 60
DB 25 QMTQSPSSLSASVGDRTVITTCRASQGISINLTWYQKRGKAPKLLIYAASSLQGVPSRF 84
QY 61 SGGSGYTDFTLITSLQFEDSATYTCQOANSFPYTFGGQTKVEIKR 105
DB 85 SGGSGGTFTLITSLQFEDSATYTCLOQNSYSTLTTFGGQTKVEIKR 129

RESULT 6
KV1G HUMAN STANDARD; PRT; 108 AA.
ID P01599;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Gal.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J.; Watanabe S.; Hilechmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I.1."
RL Hoppe-Seiler's Z. Physiol. Chem. 354:1503-1504 (1973).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01867; KIHGGL.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match
Best Local Similarity 77.0%; Score 423; DB 1; Length 108;
Matches 83; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLMAYOHQPGKAPKLLIYASASSLSQGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITTCRASQGISIRNDLTWYQKRGKAPKLLIYAASSLQGVPSRF 62
QY 61 SGGSGYTDFTLITSLQFEDSATYTCQOANSFPYTFGGQTKVEIKR 106
DB 63 SGGSGGTFTLITSLQFEDPATYTCLOQNSYSPMTFGQTKVEIKR 108

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RESULT 7
KV1L_HUMAN          STANDARD;          PRT;          108 AA.
ID   KV1L_HUMAN
AC   P01600;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DE   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Hae.
OS   Homo sapiens (human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71032830; PubMed=4097974;
RA   Watanabe S., Hlischmann N.;
RT   "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT   chain of subgroup I (Bence-Jones Protein Hae): subdivision within
RT   subgroups."
RL   Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC   -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR   HSSP; P01607; 1WTU.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; P:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Iq-like.
DR   InterPro; IPR003006; Iq_MHC.
DR   InterPro; IPR003596; Iq_V.
DR   Pfam; PF00047; Iq; 1.
DR   SMART; SM00406; IqV; 1.
DR   PROSITE; PS00835; Iq_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN 1 23 FRAMEWORK-1.
FT   DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN 35 49 FRAMEWORK-2.
FT   DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN 57 88 FRAMEWORK-3.
FT   DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN 98 107 FRAMEWORK-4.
FT   DISULFID 23 88 BY SIMILARITY.
FT   NON_TER 108 108
SQ   SEQUENCE 108 AA; 11671 MW; 08D3A6160BD0618 CRC64;
Query Match 77.0%; Score 423; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 4,4e-37;
Matches 83; Conservative 12; Mismatches 11; Indels 0; Gaps 0;
QY 1 ELTQSPSSVSASVGVDRVTITCRASQGISLWLYQHQPCKAKLLIYSASSLSQGVPSRF 60
DB 3 QMTQSPSSLSASVGVDRVTITCRASQGISLWLYQHQPCKAKLLIYSASSLSQGVPSRF 62
QY 61 SSGSGYTFDPSLTITSSLOFEDSATYCCQANSPTFGQGTKEIK 106
DB 63 SSGSGTFTLTITSSLOPEDFATYYCQQNYITPTSSGQTRVEIK 108
RESULT 8
KV1L_HUMAN          STANDARD;          PRT;          108 AA.
ID   KV1L_HUMAN
AC   P01558;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DE   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region EU.
OS   Homo sapiens (human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.

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RX   MEDLINE=71064023; PubMed=5489770;
RA   Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT   acid sequence of the light chain."
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds."
RL   Biochemistry 9:3188-3196(1970).
CC   -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   HSSP; P01607; 1REI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; P:antigen binding activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Iq-like.
DR   InterPro; IPR003006; Iq_MHC.
DR   InterPro; IPR003596; Iq_V.
DR   Pfam; PF00047; Iq; 1.
DR   SMART; SM00406; IqV; 1.
DR   PROSITE; PS00835; Iq_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN 1 23 FRAMEWORK-1.
FT   DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN 35 49 FRAMEWORK-2.
FT   DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN 57 88 FRAMEWORK-3.
FT   DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN 98 107 FRAMEWORK-4.
FT   DISULFID 23 88
FT   NON_TER 108 108
SQ   SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;
Query Match 76.3%; Score 419; DB 1; Length 108;
Best Local Similarity 76.2%; Pred. No. 1.1e-36;
Matches 80; Conservative 13; Mismatches 12; Indels 0; Gaps 0;
QY 1 ELTQSPSSVSASVGVDRVTITCRASQGISLWLYQHQPCKAKLLIYSASSLSQGVPSRF 60
DB 3 QMTQSPSSLSASVGVDRVTITCRASQGISLWLYQHQPCKAKLLIYSASSLSQGVPSRF 62
QY 61 SSGSGYTFDPSLTITSSLOFEDSATYCCQANSPTFGQGTKEIK 106
DB 63 SSGSGTFTLTITSSLOPEDFATYYCQQNSDKMFGQGTKEIK 107
RESULT 9
KV1L_HUMAN          STANDARD;          PRT;          108 AA.
ID   KV1L_HUMAN
AC   P01604;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DE   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Kue.
OS   Homo sapiens (human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79237924; PubMed=112021;
RA   Eulitz M., Kley H.-P., Zeitler H.-J.;
RT   "The primary structure of the Bence-Jones protein Kue. The amino acid
RT   sequence of the variable part of a human L-chain of the kappa-type."
RL   Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
CC   -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR   HSSP; P01607; 1REI.

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DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90EA98 CRC64;
 Query Match 76.3%; Score 419; DB 1; Length 108;
 Best Local Similarity 73.6%; Pred. No. 1.1e-36;
 Matches 78; Conservative 16; Mismatches 12; Indels 0; Gaps 0;
 QY 1 ELTOSPSVSASVGDRTTTCRASQGISMLAWQHOGKAPKLLIYSASSLSQGVPSRF 60
 DB 3 QMTOSPSLSASVGDRTTTCRASQGISMLAWQHOGKAPKLLIYSASSLSQGVPSRF 62
 QY 61 SSGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQGTKEIKR 106
 DB 63 SSGSGGTDTFTTISLQFEDSATYCCQANSFPYTFGQGTKEIKR 108
 RESULT 10
 KVL0 HUMAN STANDARD; PRT; 108 AA.
 ID KVL0 HUMAN
 AC P01507;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-I region Rel.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RX MEDLINE=76023758; PubMed=809329;
 RA Palm W., Hilschmann N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin
 RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
 RT and characterization of the tryptic peptides; the complete amino acid
 RT sequence of the protein; a contribution to the elucidation of the
 RT three-dimensional structure of antibodies, in particular their
 RT combining site.";
 RT Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=76039968; PubMed=1182131;
 RA Bpp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
 RT "The molecular structure of a dimer composed of the variable portions
 RT of the Bence-Jones protein REI refined at 2.0-A resolution.";
 RT Biochemistry 14:4943-4952(1975).
 CC -1- MISCELLANEOUS; THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 CC -1- MISCELLANEOUS; THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A81663; KIHURE.
 DR PDB; 1REI; 17-FEB-84.
 DR PDB; 1AR2; 12-NOV-97.
 DR PDB; 1BMW; 29-DEC-99.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT STRAND 4 7
 FT STRAND 10 13
 FT STRAND 15 16
 FT STRAND 19 25
 FT STRAND 30 31
 FT STRAND 33 38
 FT STRAND 40 41
 FT STRAND 44 49
 FT STRAND 50 52
 FT STRAND 53 54
 FT STRAND 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT STRAND 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 85 90
 FT STRAND 97 98
 FT STRAND 102 106
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;
 Query Match 75.8%; Score 416; DB 1; Length 108;
 Best Local Similarity 75.5%; Pred. No. 2.3e-36;
 Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
 QY 1 ELTOSPSVSASVGDRTTTCRASQGISMLAWQHOGKAPKLLIYSASSLSQGVPSRF 60
 DB 3 QMTOSPSLSASVGDRTTTCRASQGISMLAWQHOGKAPKLLIYSASSLSQGVPSRF 62
 QY 61 SSGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQGTKEIKR 106
 DB 63 SSGSGGTDTFTTISLQFEDSATYCCQANSFPYTFGQGTKEIKR 108
 RESULT 11
 KVLB HUMAN STANDARD; PRT; 108 AA.
 ID KVLB HUMAN
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-I region AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RX MEDLINE=72189444; PubMed=5028201;
 RA Schiechl H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 RT protein AU)."
 RT Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY.

RX MEDLINE=77022433; PubMed=1234024;
RA Fehlgamer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Seigelmann W., Schramm H.J.,
RT "The structure determination of the variable portion of the
RT Bence-Jones protein Au."
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A91653; KIHUV.
DR PDB; 1JVS; 30-JAN-02.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E801187BE6F6B9 CRC64;

Query Match 75.2%; Score 413; DB 1; Length 108;
Best Local Similarity 75.5%; Pred. No. 4.7e-36;
Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSAVGDRTTTCRASQGISLWLYQHOPKAPKLLIYSASSLSQGVPSRF 60
DB 3 QMTQSPSSLSASVGRVITTCQASQDSDILNMQKPGAPKLLIYDASNLSSGVPSRF 62
61 SSGSGYTDFTLTISLQPEDSATYVCOQANSFPYFGQTKVEIKR 106
DB 63 SSGSGYTDFTLTISLQPEDSATYVCOQYVLPWTFQGTKEIKR 108

RESULT 12
KVLM_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.,
RT "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities."
RL Scand. J. Immunol. 5:677-684(1976).
CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN FOM V-IT KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01871; KIHUV.

DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 74.7%; Score 410; DB 1; Length 108;
Best Local Similarity 72.6%; Pred. No. 9.7e-36;
Matches 77; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSAVGDRTTTCRASQGISLWLYQHOPKAPKLLIYSASSLSQGVPSRF 60
DB 3 QMTQSPSSLSASVGRVITTCQASQDSDILNMQKPGAPKLLIYDASNLSSGVPSRF 62
61 SSGSGYTDFTLTISLQPEDSATYVCOQANSFPYFGQTKVEIKR 106
DB 63 SSGSGYTDFTLTISLQPEDSATYVCOQYVLPWTFQGTKEIKR 108

RESULT 13
KVLE_HUMAN STANDARD; PRT; 108 AA.
AC P01587;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region DEE.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72053133; PubMed=5124396;
RA Milstein C.P., Deverson E.V.,
RT "The amino acid sequence of a human kappa light chain."
RL Biochem. J. 123:945-958(1971).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR; A01865; KIHUV.
DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;


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Oy      61 SSGSGYCTDPSLTITSSLQFEDSATYYCCQANSFPYTFGGQTKVEIKR 106
        |||::|||:|||||::|:|||||:|
Db      63 SSGSGFTDFTTISGLQPEDATYYCQDYDTLPRTFGGQTKLEIKR 108

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Db 63 SGTSGTDFTFTISSLPEDIATYCCQFDNLP LTFGGTKVDfKR 108

Search completed: February 10, 2004, 18:36:31
Job time : 5.94242 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	437	79.6	108	4	Q9UJ70	Q9UJ70 homo sapien
2	437	79.6	108	4	Q9UJ77	Q9UJ77 homo sapien
3	434	79.1	108	4	Q9UJ79	Q9UJ79 homo sapien
4	426.5	77.7	107	4	Q96S49	Q96S49 homo sapien
5	411.5	75.0	107	4	Q9UJ81	Q9UJ81 homo sapien
6	384	69.9	214	11	Q9UJ1A5	Q9UJ1A5 mus musculus
7	382	69.6	108	4	Q9UJ83	Q9UJ83 homo sapien
8	377	68.7	234	4	Q8NEX1	Q8NEX1 homo sapien
9	377	68.7	234	11	Q8R062	Q8R062 mus musculus
10	368	66.7	116	4	Q96P6F6	Q96P6F6 homo sapien
11	366	67.0	108	11	Q8VJ0J0	Q8VJ0J0 mus musculus
12	365	66.5	233	11	Q91WS9	Q91WS9 mus musculus
13	365	66.5	234	11	Q91WPF8	Q91WPF8 mus musculus
14	364.5	66.4	109	4	Q9UJ78	Q9UJ78 homo sapien
15	364	66.3	234	11	Q8VCPO	Q8VCPO mus musculus
16	362	65.9	298	11	Q9QYF0	Q9QYF0 mus musculus

17	360.5	65.7	114	11	08K1F1
18	357.5	65.1	109	4	09ULB5
19	355	64.7	109	11	0920E6
20	354	64.5	111	11	0920E9
21	353.5	64.4	112	11	08K1F3
22	352.5	64.2	112	11	08K1F2
23	351	63.9	107	11	09J1B4
24	346.5	63.1	134	11	08VDD0
25	338.5	61.7	106	5	09U410
26	337.5	61.5	109	4	09ULB6
27	332	60.5	99	11	09J174
28	324.5	59.1	241	11	0921A6
29	324	59.0	107	11	09ERZ9
30	323	58.8	127	11	0925S9
31	322	58.7	101	11	09J178
32	320.5	58.4	112	11	08K1F0
33	316.5	57.7	238	11	095937
34	310	56.5	103	11	09J1B0
35	309.5	56.4	235	11	09J1W2
36	307	55.9	97	11	09J176
37	304	55.4	234	11	08R028
38	300.5	54.7	239	11	08VC16
39	300.5	54.7	239	11	08VC55
40	295.5	53.8	239	4	08NKK0
41	291.5	53.1	239	4	08TCD0
42	291.5	53.1	239	11	08K0F8
43	286.5	52.2	104	11	09J1B2
44	285	51.9	109	6	09J0M5
45	285	51.9	114	4	09ULB0
					08K1F1 mus musculus
					09ulb5 homo sapien
					0920e6 mus musculus
					0920e9 mus musculus
					08K1f3 mus musculus
					08K1f2 mus musculus
					09J1B4 mus musculus
					08vdd0 mus musculus
					09u410 schistosoma
					09ulb6 homo sapien
					09J174 mus musculus
					0921a6 mus musculus
					09erz9 mus musculus
					0925s9 mus musculus
					09J178 mus musculus
					08K1f0 mus musculus
					0959m7 mus musculus
					09J1B0 mus musculus
					09J1W2 mus musculus
					09J176 mus musculus
					08r028 mus musculus
					08vc16 mus musculus
					08vc55 mus musculus
					08nkk0 homo sapien
					08tcd0 homo sapien
					08K0f8 mus musculus
					09J1B2 mus musculus
					09J0M5 oryctolagus
					09ulb0 homo sapien

ALIGNMENTS

RESULT 1	
Q9UL70	
ID	PRELIMINARY;
Q9UL70	PRT; 108 AA

DT 01-MAY-2000 (TREMBLref1. 13, Created)
DT 01-MAY-2000 (TREMBLref1. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLref1. 23, Last annotation update)
DT Myosin-reactive immunoglobulin light chain variable region
DS (fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT feus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035044; AAD55280.1; -.
 DR HSSP; P01607; IREI.
 DR InterPro; IPR007110; IG_1-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR NON_TER 1
 FT 108 108
 FT SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

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Query Match      79.6% Score 437; DB 4; Length 108;
Best Local Similarity 80.2% Pred. No. 6.1e-39;
Matches      85; Conservative 11; Mismatches 10; Indels 0; Gaps 0
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Gy 1 ELTSPSSVASVDRTVITCRASGIGISMTLAWYOHQPKAPKLLIYSASSIQSGVPSEF 60
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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Db 3 QMTGSPSSLSASVGDVRVITITORASGGSINYLAWYQKKGKVKPKSLIYAASLTSGVPSRF 62
Qy 61 SGGVGTDPFSLTISLSLQPEDSATYTYCCQANSPFTYFGGTKEIKR 106
Db 63 SGGSGGTDPFTLTISLSLQPEDVAITYCCQKYNASPFRTGEGTKLEIKR 108

RESULT 2
Q9UL77 PRELIMINARY; PRT; 108 AA.
ID Q9UL77
AC Q9UL77;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive Immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 79.6%; Score 437; DB 4; Length 108;
Best Local Similarity 81.1%; Pred. No. 6,1e-39;
Matches 86; Conservative 10; Mismatches 10; Indels 0; Gaps 0.

Qy 1 ELTGSPSSVASVGDVRVITTCRASGGSISWYLAWYQHPGKAPKLLIYSASSLQGVPSRF 60
Db 3 QMTGSPSSLSASVGDVRVITTCRASGGSISYLNWYQKPKOKAPNLLIYAASLTSGVPSRF 62
Qy 61 SGGVGTDPFSLTISLSLQPEDSATYTYCCQANSPFTYFGGTKEIKR 106
Db 63 SGGSGGTDPFTLTISLSLQPEDVAITYCCQKYNASPFRTGEGTKLEIKR 108

RESULT 3
Q9UL79 PRELIMINARY; PRT; 108 AA.
ID Q9UL79
AC Q9UL79;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Myosin-reactive Immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."

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BL	Clin. Immunol.	Immunopathol.	87.184-192(1998).
DR	EMBL:	AF035035;	AAD6271.1; -
DR	HSSP:	P01607;	IRED.
DR	InterPro:	IPR007110;	IG_1ike.
DR	InterPro:	IPR003006;	IG_MHC.
DR	InterPro:	IPR003596;	IG_v.
DR	Pfam:	PF00047;	IG; 1.
DR	SMART:	SMO0406;	IGv; 1.
DR	PROSITE:	PS50835;	IG_LIKE; 1.
FT	NON_TER	1	1
FT	NON_TER	108	108
SO	SEQUENCE	108 AA;	11787 MW; DB545F19724FB4E CRC64;
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Qy	Query Match	79.1%;	Score 434; DB 4; Length 108;
	Best Local Similarity	81.0%;	Pred. No. 1.3e-38;
	Matches	85; Conservative	9; Mismatches 11; Indels 0; Gaps 0;
Dd			
Qy		62	GSGYGTDFSLTISLQPEDSATYYCOQANSFPPTFGGKTVEIKR 106
Dd		64	GSGSGTDFTLTITLSCTLOSEDEPATYYCQCYSPFPPTFGGKTVEIKR 108
<hr/>			
RESULT 4			
ID	Q96SA9	PRELIMINARY;	PRT; 107 AA.
AC	Q96SA9;		
DT	01-DEC-2001	(TREMBLrel. 19,	Created)
DT	01-DEC-2001	(TREMBLrel. 19,	Last sequence update)
DT	01-MAR-2003	(TREMBLrel. 23,	Last annotation update)
DE	Anti-streptococcal/anti-mysin immunoglobulin kappa light chain variable region (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=98375893; Pubmed=9712075;		
RX	Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;		
RT	"Molecular analysis of polyclonal monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes."		
RL	J. Immunol. 161:2020-2031(1998).		
DR	EMBL: U96396; AAB68785.1; -		
DR	InterPro: IPR007110;		
DR	InterPro: IPR003006;		
DR	InterPro: IPR003596;		
DR	Pfam: PF00047;		
DR	SMART: SMO0406;		
DR	PROSITE: PS50835;		
FT	NON_TER	1	1
FT	NON_TER	107	107
SO	SEQUENCE	107 AA;	11520 MW; 4BB43E9C5B577F16 CRC64;
<hr/>			
Qy	Query Match	77.7%;	Score 426.5; DB 4; Length 107;
	Best Local Similarity	82.1%;	Pred. No. 7.9e-38;
	Matches	87; Conservative	8; Mismatches 10; Indels 1; Gaps 1;
Dd			
Qy		61	ELTGSPSSVSASVGDVYTITCRASOGISSWLAHYQHOPGRAPKLLIYSASSLGCVPSRF 60
Dd		3	QMTGPSPLSASVDVRYITCRASOGISSSYLMNYQOKRGKAPKLLIYAASSTLGCVPSRF 62
Qy		61	GSGYGTDFTLTISLQPEDSATYYCOQANSFPPTFGGKTVEIKR 106
Dd		63	GSGSGTDFTLTISLQPEDPATYYCQCYSPFPPTFGGKTVEIKR 107

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ID 09UL81 PRELIMINARY; PRT; 107 AA.
AC 09UL81;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=96277139; PubMed=9614934;
RA Wu X., Lin B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; Ig_1-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 75.0%; Score 411.5; DB 4; Length 107;
Best Local Similarity 77.4%; Pred. No. 3.1e-36;
Matches 82; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

Qy 1 ELTQSPSSVSAVSGRVITTCRASQGISWMLAWYOHQPKKLIYSASLSQGVPSRF 60
Db 3 QLTQSPSSVSAVSGRVITTCRASQGISWMLAWYOHQPKKLIYSASLSQGVPSRF 62

Qy 61 GSGGVTDFSLTISLQFEDSATYVCOQANSFPYFGQTKVEIKR 106
Db 63 GSGSGGTDFTLTISLQFEDPATYVCOQANSYSLALTFPGTKVDIKR 107

RESULT 6
Q9RLA5 PRELIMINARY; PRT; 214 AA.
AC Q9RLA5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig_1-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 1

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FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 69.9%; Score 384; DB 11; Length 214;
Best Local Similarity 67.0%; Pred. No. 6e-33;
Matches 71; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSAVSGRVITTCRASQGISWMLAWYOHQPKKLIYSASLSQGVPSRF 60
Db 3 QLTQSPSSVSAVSGRVITTCRASQGISWMLAWYOHQPKKLIYSASLSQGVPSRF 62

Qy 61 GSGGVTDFSLTISLQFEDSATYVCOQANSFPYFGQTKVEIKR 106
Db 63 GSGSGGTDFTLTISLQFEDPATYVCOQANSYSLALTFPGTKVDIKR 108

RESULT 7
Q9UL83 PRELIMINARY; PRT; 108 AA.
AC 09UL83;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=96277139; PubMed=9614934;
RA Wu X., Lin B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig_1-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 69.6%; Score 382; DB 4; Length 108;
Best Local Similarity 65.7%; Pred. No. 4.3e-33;
Matches 69; Conservative 21; Mismatches 15; Indels 0; Gaps 0;

Qy 2 LTQSPSSVSAVSGRVITTCRASQGISWMLAWYOHQPKKLIYSASLSQGVPSRF 61
Db 4 MTQSPSSVSAVSGRVITTCRASQGISWMLAWYOHQPKKLIYSASLSQGVPSRF 63

Qy 62 GSGGVTDFSLTISLQFEDSATYVCOQANSFPYFGQTKVEIKR 106
Db 64 GSGSGGTDFTLTISLQFEDPATYVCOQANSYSLALTFPGTKVDIKR 108

RESULT 8
Q9NEK1 PRELIMINARY; PRT; 234 AA.
AC Q9NEK1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```


RESULT 15

```

O8VCP0 PRELIMINARY; PRT; 234 AA.
ID O8VCP0
AC O8VCP0;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 25.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC019474; AA19474.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match 66.3%; Score 364; DB 11; Length 234;
Best Local Similarity 65.1%; Pred. No. 9e-31;
Matches 69; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSYGDRVTITCRASQGISWLAHYOHOPGKAPKLLIYSASLSQGVPSRF 60
DB 23 QLTQSPASLSASVGERVTITCRASENIYSILANYQOKGKSPQLVYNAKTLADGVPSRF 82
QY 61 SSGSGYGTDFSLTISLQFEDSATYCCQANSPPYTFGGTKV2IKR 106
DB 83 SSGSRSGTQFSLKINSIQPEDFGSYCCOHSGIGIPFTFGSGTKLEIKR 128

```

Search completed: February 10, 2004, 18:39:23
 Job time : 25.0545 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 17:46:18 : Search time 31.9606 Seconds
(without alignments)
526.430 Million cell updates/sec

Title: US-10-027-725a-12

Perfect score: 549
Sequence: 1 ELTQSPSPSVASVGDRTVIT.....QQANSFPTFGQTKVEIKR 106

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
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- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
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- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	527	96.0	106	23	ABG30450 Human IGE Fab clone
2	518	94.4	233	21	ABAB03713 Immunoglobulin kappa
3	485	88.3	107	23	ABAB07237 Anti-IL-4 and IL-1
4	484	88.2	223	24	ABJ36940 Anti-CD40 monoclon
5	478	87.1	107	22	AA665571 Amino acid sequenc
6	478	87.1	244	23	ABP45870 Human Bly5 binding
7	475	86.5	236	23	AAU74297 Anti-human ALIM m
8	474	86.3	105	23	AAO18424 Anti-CD2 antibody
9	467	85.1	107	22	AAAB72880 Human anti-HER2/ne

10	466	84.9	108	23	AAU76522
11	464.5	84.6	109	22	AAE10815
12	463	84.3	107	22	AAAG30597
13	462	84.2	107	22	AAAB72882
14	462	84.2	224	22	AAAB75040
15	460	83.8	107	15	AAAB54260
16	460	83.8	107	17	AAAO1283
17	460	83.8	107	21	AAAY95135
18	460	83.8	107	21	AAAY8244
19	460	83.8	107	22	AAAB7511
20	460	83.8	108	19	AAAW70622
21	460	83.8	108	21	AAAY82345
22	460	83.8	108	23	ABPE1191
23	460	83.8	109	23	AAU74544
24	460	83.8	110	23	AAE28149
25	460	83.8	224	22	AAAB75043
26	459	83.6	107	22	AAAB82890
27	459	83.6	109	15	AAAB47041
28	459	83.6	128	17	AAAO1527
29	459	83.6	128	18	AAAB24990
30	459	83.6	224	22	AAAB75044
31	458	83.4	109	14	AAAB30764
32	457	83.2	107	15	AAAB54305
33	457	83.2	107	17	AAAO1263
34	457	83.2	107	21	AAAY95115
35	457	83.2	107	21	AAAY8224
36	457	83.2	107	22	AAAG3663
37	457	83.2	107	22	AAAG3664
38	457	83.2	107	24	AAE28874
39	457	83.2	107	23	AAE26767
40	456	83.1	207	22	AAAG3644
41	456	83.1	241	23	AAU90948
42	455.5	83.0	109	23	AAAB76536
43	455	82.9	107	22	AAAB62087
44	455	82.9	107	22	AAAB60400
45	455	82.9	107	22	AAAB1585

ALIGNMENTS

RESULT 1					
ID	ABG30450	standard; Protein; 106 AA.			
XX	ABG30450;				
AC	ABG30450;				
XX	21-OCT-2002	(first entry)			
DT					
XX					
DE		Human IGE Fab clone 100 light chain protein.			
XX					
XX		Human; fab; anti-allergic; vaccine; grass pollen; Phi p 2;			
KW		timothy grass pollen allergen; passive immunotherapy.			
XX					
OS		Homo sapiens.			
XX					
FH		Location/Qualifiers			
FT	Key	1..21			
FT	Region	/note= "FRI region"			
FT	Region	22..32			
FT	Region	/note= "CDR1 region"			
FT	Region	33..47			
FT	Region	/note= "FR2 region"			
FT	Region	48..54			
FT	Region	/note= "CDR2 protein"			
FT	Region	55..86			
FT	Region	/note= "FR3 region"			
FT	Region	87..95			
FT	Region	/note= "CDR2 region"			
FT	Region	96..104			
FT	Region	/note= "FR4 region"			
FT	Misc-difference	65			
FT		/note= "Encoded by TCT"			

Anti-Interleukin-1
Human antibody CAT
Human anti-Rh(D) c
Human anti-HER2/ne
TRO005 Humab kappa
Anti-HIV gp120 imm
VL region of HIV n
Anti-gp120 antibody
Anti-gp120 antibody
Light chain variab
Human consensus fr
Human consensus se
Human anti-VEGF an
Human subgroup lig
Human consensus va
TRO005 Humab kappa
Anti-human CD154 a
Sequence of the co
Monoclonal antibod
TRO005 Humab kappa
Consensus humanise
Anti-HIV gp120 imm
VL region of HIV n
Anti-gp120 antibody
Human anti-Rh(D) a
Human anti-Rh(D) a
Human KDR (VEGFR-2
VEGF binding relat
Human anti-Rh(D) a
Insulin/insulin-li
HCV E1 antigen mon
Human VI consensus
Consensus human li
Human variable lig

XX MO200253595-A1.
 XX 11-JUL-2002.
 XX 27-DEC-2001; 2001MO-SE02908.
 XX 29-DEC-2000; 2000SE-0004692.
 XX (PHAA) PHARMACIA DIAGNOSTICS AB.
 XX Flicker S, Steinberger P, Kraft D, Valenta R;
 XX MPI: 2002-583604/62.
 XX N-PSDB; ABR9642.
 XX
 XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
 PT variable region of group 2 allergen specific-human IGE Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for
 PT environmental allergen detection -
 XX
 XX Disclosure; Page 41; 45pp; English.
 XX
 XX This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IGE Fabs and methods for their use. The proteins
 CC of the invention may have antiallergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's
 CC IGE antibodies to Phi p 2 (a major timothy grass pollen allergen).
 CC The group 2 allergen-specific Fabs of the invention may be useful for
 CC environmental allergen detection and for standardisation of allergen
 CC extracts. The Fabs - or a vaccine against a type I allergy is useful for
 CC passive immunotherapy of type I allergy. It is also useful for
 CC diagnosing a type I allergy. The allergen-specific Fabs of the invention
 CC are useful for inter alia, diagnosis, therapy and prevention of type
 CC I allergy. They are also useful for identification of group 2
 CC allergen-containing pollen and may be used for blocking the binding of
 CC grass pollen allergic patients IGE antibodies to Phi p 2. The present
 CC sequence represents the human Igg fab, clone 100 light chain protein of
 CC the invention.
 XX
 XX Sequence 106 AA;
 SQ
 XX
 XX Query Match 96.0%; Score 527; DB 23; Length 106;
 Best Local Similarity 97.2%; Pred. No. 1.4e-30;
 Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ELTQSPSSVSASVGVDRVTITCRASOGISSWLMAYOHOPKAPKLLIYSASSLSQGVPSRF 60
 DB 1 ELTQSPSSVSASVGVDRVTITCRASOGISSWLMAYOHOPKAPKLLIYSASSLSQGVPSRF 60
 QY 61 SSGSGYGTDFSLTISLQPEDSATYTYCOQANSFPYTFGQGTKEIKR 106
 DB 61 SSGSGYGTDFSLTISLQPEDSATYTYCOQANSFPYTFGQGTKEIKR 106
 RESULT 2
 ABB03713
 ID AAB03713 standard; protein; 233 AA.
 XX
 XX AAB03713;
 XX
 XX 04-OCT-2000 (first entry)
 XX
 XX Immunoglobulin kappa amino acid sequence fragment.
 DE
 XX Aortic aneurysm-associated antigen protein; AAP; microfibrillar protein;
 XX abdominal aortic aneurysm disease; treatment; detect; tolerance;
 KW immunoglobulin kappa, Igk.
 KM
 XX
 XX Unidentified.
 OS
 XX
 XX US6048704-A.
 PN
 XX

PD 11-APR-2000.
 XX
 XX 07-MAR-1997; 97US-0812586.
 XX
 XX 07-MAR-1996; 96US-0012976.
 XX
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 XX PA
 XX Tilson MD;
 XX
 XX MPI; 2000-316895/27.
 XX
 XX
 XX Isolated microfibrillar protein for alleviating abdominal aortic
 PT aneurysm disease is purified from human aortic tissue and binds
 PT immunoreactively with immunoglobulin -
 XX
 XX Example 3; Column 29-31; 70pp; English.
 XX
 XX The present invention relates to an isolated microfibrillar protein of
 CC approximately 40kD. The protein is isolated from human aortic tissue and
 CC binds immunoreactively with immunoglobulin purified from human abdominal
 CC aortic aneurysm (AAA) tissue. The protein is referred to as aortic
 CC aneurysm-associated antigenic protein (AAP). The protein is capable of
 CC forming a disulphide bonded dimer. The protein is immunoreactive with
 CC human kappa immunoglobulin. Also included in the invention are
 CC recombinantly produced human AAA protein. AAP shows regions of homology
 CC with the bovine microfibril associated glycoprotein MFAP-4 and also with
 CC fibrinogen and vitronectin. The isolated microfibrillar protein is useful
 CC for alleviating abdominal aortic aneurysm (AAA) disease and detecting the
 CC presence of AAA-associated immunoglobulin bound to the human aortic
 CC tissue. Antibodies directed against AAP can be used to detect AAA
 CC disease. The recombinant protein can be used to induce tolerance to
 CC antigenic AAP protein in the subject e.g. human. This sequence represents
 CC an immunoglobulin kappa amino acid sequence. The sequence shares homology
 CC with the AAP of the invention, it was used to identify and characterise
 CC AAP.
 XX
 XX Sequence 233 AA;
 SQ
 XX
 XX Query Match 94.4%; Score 518; DB 21; Length 233;
 Best Local Similarity 96.2%; Pred. No. 1.2e-29;
 Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ELTQSPSSVSASVGVDRVTITCRASOGISSWLMAYOHOPKAPKLLIYSASSLSQGVPSRF 60
 DB 23 ELTQSPSSVSASVGVDRVTITCRASOGISSWLMAYOHOPKAPKLLIYSASSLSQGVPSRF 82
 QY 61 SSGSGYGTDFSLTISLQPEDSATYTYCOQANSFPYTFGQGTKEIKR 106
 DB 83 SSGSGYGTDFSLTISLQPEDSATYTYCOQANSFPYTFGQGTKEIKR 128
 RESULT 3
 ABB07237
 ID ABB07237 standard; protein; 107 AA.
 XX
 XX ABB07237;
 XX
 XX 26-MAR-2002 (first entry)
 XX
 XX Anti-IL-4 and IL-13 receptors MAb 63 light chain variable region.
 DE
 XX Human; antibody; interleukin; IL-4; antagonist; receptor; IL-4 receptor;
 KW antidiabetic; dermatological; antitumor; antiinflammatory; cytostatic;
 KW antiskinning; immunosuppressive; tuberculostatic; ophthalmological;
 KW IL-13; antianemic; antichryd.
 KM
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 XX Key 24..34
 XX Region /note="complementarity determining region (CDR) 1"
 FT Region 50..56
 FT

FT /note= "complementarity determining region (CDR) 2"
 FT 89..97
 FT /note= "complementarity determining region (CDR) 3"
 XX
 XX Region
 XX
 XX WO200192340-A2.
 XX
 XX 06-DEC-2001.
 XX
 XX 25-MAY-2001; 2001WO-US17094.
 XX
 XX 26-MAY-2000; 2000US-0579808.
 XX 19-SEP-2000; 2000US-0665343.
 XX 15-FEB-2001; 2001US-0785934.
 XX 01-MAY-2001; 2001US-0847816.
 XX
 XX (IMMUNEX CORP.
 XX
 XX Plueneke JD;
 XX
 XX WPI: 2002-114332/15.
 XX N-PSDB; ABA94337.
 DR
 XX
 XX Novel human antibody which binds human interleukin (IL)-4 receptor and
 PT is capable of inhibiting IL-4 induced biological activity, functions as
 PT IL-4 antagonist and is useful for treating septic arthritis,
 PT scleroderma
 PT
 XX Claim 3; Page 82; 85pp; English.
 PS
 XX
 XX The invention relates to a human antibody (an interleukin (IL)-4
 CC antagonist) (I) that binds human IL-4 receptor (IL-4R), and is capable of
 CC inhibiting an IL-4-induced biological activity. (I) is also useful for
 CC inhibiting both IL-4-induced biological activity and IL-13-induced
 CC biological activity in vivo in a human, and for treating septic arthritis
 CC in a human afflicted with septic arthritis. (I) is also used for treating
 CC conditions such as septic/reactive arthritis, dermatitis herpetiformis,
 CC urticaria (especially chronic idiopathic urticaria), ulcers, gastric
 CC inflammation, mucosal inflammation, ulcerative colitis, Crohn's disease,
 CC inflammatory bowel disease, other disorders of the digestive system in
 CC which IL-4 plays a role (e.g. IL-4-induced inflammation of part of the
 CC gastrointestinal tract), conditions in which IL-4-induced barrier
 CC disruption plays a role (e.g. conditions characterized by decreased
 CC epithelial barrier function in the lung or gastrointestinal tract),
 CC scleroderma, hypertrophic scarring, whipple's disease, benign prostatic
 CC hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to
 CC medication, Kawasaki disease, sickle cell disease or crisis, Churg-
 CC Strauss syndrome, Grave's disease, pre-eclampsia, Sjogren's syndrome,
 CC autoimmune lymphoproliferative syndrome, autoimmune hemolytic anemia,
 CC Barrett's esophagus, autoimmune uveitis, tuberculosis, nephrosis,
 CC pemphigus vulgaris or bullous pemphigoid (autoimmune blistering
 CC diseases), and myasthenia gravis (an autoimmune muscular disease). IL-4
 CC antagonists also find use as adjuvants to allergy immunotherapy and as
 CC vaccine adjuvants, especially when directing the immune response toward
 CC a TH1 response would be beneficial in treating or preventing the disease.
 CC The present sequence represents an anti-IL-4 receptor and anti-IL-13
 CC receptor monoclonal antibody (MAB) 63 light chain variable region.
 CC
 XX
 XX Sequence 107 AA;
 SQ
 Query Match 88.3%; Score 485; DB 23; Length 107;
 Best Local Similarity 88.6%; Pred. No. 1.4e-27;
 Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 ELTQSPSSVSASVGRVITTCRASQGISSTWLMWYOHQPKAKPLIYASSTLSQGVPSRF 60
 Db 3 QMTQSPSSVSASVGRVITTCRASQGISSTWLMWYOHQPKAKPLIYASSTLSQGVPSRF 62
 Oy 61 SSGSGGTDFSLTTLISLQFEDSATYYTCQANSFPYFGGTVEIKR 105
 Db 63 SSGSGGTDFSLTTLISLQFEDSATYYTCQANSFPYFGGTVEIKR 107
 RESULT 4

ABJ36940
 ID ABJ36940 standard; Protein; 223 AA.
 XX
 XX ABJ36940;
 AC
 XX
 XX 01-MAY-2003 (first entry)
 DT
 XX
 XX Anti-CD40 monoclonal antibody related protein SEQ ID No 66.
 DE
 XX
 XX Antiallergic; haemostatic; immunomodulator; cytostatic; antibody;
 KW human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma;
 KW dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;
 KW immunocytotoxic; anti-tumour agent; immunosuppressant; allergy;
 KW autoimmune disease; coagulation factor VIII inhibitor; anti-CD40.
 XX
 XX Unidentified.
 OS
 XX
 XX WO200288186-A1.
 XX
 XX 07-NOV-2002.
 PD
 XX
 XX 26-APR-2002; 2002WO-JP04292.
 PF
 XX
 XX 27-APR-2001; 2001WO-US3672.
 PR 11-MAY-2001; 2001JP-0142482.
 PR 05-OCT-2001; 2001JP-0310535.
 PR 26-OCT-2001; 2001US-0040244.
 XX
 XX (KIRI) KIRIN BEER KK.
 PA
 XX
 XX Mikayama T, Yoshida H, Force WR, Chen X, Takahashi N;
 PI
 XX
 XX WPI: 2003-120463/11.
 DR N-PSDB; APT31882.
 XX
 XX Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40,
 PT or functional fragment, is useful in the treatment of e.g. autoimmune
 PT diseases or cancer
 PT
 XX
 XX Claim 15; Page 60; 94pp; Japanese.
 PS
 XX
 XX The invention relates to an antibody to human CD40, or its functional
 CC fragment, has at least one of the following properties: acting on
 CC dendritic cells to produce IL-12 in the presence of LPS
 CC (lipopolysaccharide) and IFNgamma (interferon gamma); acting on dendritic
 CC cells to activate maturity of the dendritic cells with high G28-5
 CC antibody; and activating CD95 expression with high G28-5 antibody against
 CC B cell line. Such antibodies or functional fragments can be used as
 CC immunocytotoxic, anti-tumour agents, immunosuppressants, and as remedies
 CC for autoimmune diseases, allergy or coagulation factor VIII inhibitors
 CC syndrome. This sequence represents a protein relating to the anti-CD40
 CC monoclonal antibody of the invention.
 CC
 XX
 XX Sequence 223 AA;
 SQ
 Query Match 88.2%; Score 484; DB 24; Length 223;
 Best Local Similarity 87.7%; Pred. No. 3.1e-27;
 Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
 Oy 1 ELTQSPSSVSASVGRVITTCRASQGISSTWLMWYOHQPKAKPLIYASSTLSQGVPSRF 60
 Db 25 QMTQSPSSVSASVGRVITTCRASQGISSTWLMWYOHQPKAKPLIYASSTLSQGVPSRF 84
 Oy 61 SSGSGGTDFSLTTLISLQFEDSATYYTCQANSFPYFGGTVEIKR 106
 Db 85 SSGSGGTDFSLTTLISLQFEDSATYYTCQANSFPYFGGTVEIKR 130
 RESULT 5
 AAG65571
 ID AAG65571 standard; protein; 107 AA.
 XX
 XX AAG65571;
 AC

XX 30-NOV-2001 (first entry)
 XX Amino acid sequence of protein seq Id No. 96.
 DE Gene library; immunoglobulin; antibody library; human.
 XX Homo sapiens.
 OS WO200162907-A1.
 XX 30-AUG-2001.
 PD 22-FEB-2001; 2001WO-JP01298.
 PF 22-FEB-2000; 2000JP-0050543.
 XX (MED1-) MEDICAL & BIOLOGICAL LAB CO LTD.
 PA Kurokawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
 PI Okuno Y, Shireki K;
 XX MPI; 2001-565420/63.
 DR N-PSDB; AAH47735.
 XX Producing gene libraries and antibody libraries, involves selecting a
 PT light chain that binds to a heavy chain product to produce a functional
 PT formation, and producing a gene library of the light chain variable
 PT regions -
 XX Examples; p 172; 181pp; Japanese.
 PS The invention relates to producing gene libraries, comprising
 CC immunoglobulin light and heavy variable region. The method involves
 CC selecting light chain that binds with the heavy chain product to produce
 CC a functional conformation, producing a gene library comprising a
 CC collection of these light chain variable genes, and combining with gene
 CC library of heavy chain variable genes. The method is used for production
 CC of gene and antibody libraries.
 CC
 SQ Sequence 107 AA;
 Query Match 87.1%; Score 478; DB 22; Length 107;
 Best Local Similarity 88.6%; Pred. No. 4.3e-27; Mismatches 6; Indels 0; Gaps 0;
 Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 1 ELTQSSSVASVSGDRVTTCRASOGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRR 60
 DB 3 QMTQSSSVASVSGDRVTTCRASOGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRR 62
 QY 61 GSGGYTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIK 105
 DB 63 GSGSGTDFLTITSLQPEDFATYCCQANSFPYTFGGTKVEIK 107
 RESULT 6
 ABP45870 ID ABP45870 standard; Protein; 244 AA.
 XX ABP45870;
 DT 19-AUG-2002 (first entry)
 XX Human Bly's binding scFv SEQ ID 1881.
 DE Human Bly's binding scFv SEQ ID 1881.
 XX Bly's: B lymphocyte stimulator; TNF superfamily; human; cytosolic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.
 OS Homo sapiens.

XX WO200202641-A1.
 PN 10-JAN-2002.
 PD 15-JUN-2001; 2001WO-US91110.
 PF 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 PI MPI; 2002-114799/15.
 DR Antibodies against B lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 PT Claim 1; Page 2646-2647; 3148pp; English.
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytosolic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 CC
 SQ Sequence 244 AA;
 Query Match 87.1%; Score 478; DB 23; Length 244;
 Best Local Similarity 88.6%; Pred. No. 9e-27; Mismatches 6; Indels 0; Gaps 0;
 Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 2 LTQSPSSVASVSGDRVTTCRASOGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRR 61
 DB 140 MTQSPSTLSASVGDRTVITTCRASOGISWLAHYOHOPGKAPKLLIYSASSLSQGVPSRR 199
 QY 62 GSGGYTDFSLTISLQFEDSATYCCQANSFPYTFGGTKVEIK 106
 DB 200 GSGSGTDFLTITSLQPEDFATYCCQANSFPYTFGGTKVEIKR 244
 RESULT 7
 AAU74297 ID AAU74297 standard; Protein; 236 AA.
 XX AAU74297;
 DT 12-MAR-2002 (first entry)
 XX Anti-human Allm monoclonal antibody clone Jmab-136, light chain.
 DE Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 XX Human; antirheumatic; antidiabetic; antipsoriatic;
 KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM immunosuppressive; dermatological; antirheumatic; hepatotropic;
 KM activation inducible lymphocyte immunomodulatory molecule; Allm;
 KM monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;

KM multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
 KM allergic contact-type dermatitis; chronic inflammatory dermatosis;
 KM systemic lupus erythematosus; autoimmune disorder; inflammation;
 KM graft versus host reaction; immune rejection; intestinal immunity;
 KM ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
 OS Homo sapiens.
 XX WO200187981-A2.
 XX
 XX 22-NOV-2001.
 XX
 XX 15-MAY-2001; 2001WO-JP04035.
 XX
 XX 18-MAY-2000; 2000JP-0147116.
 XX 30-MAR-2001; 2001JP-0099508.
 XX
 XX (NISR) JAPAN TOBACCO INC.
 XX
 XX Tsuji T, Tezuka K, Hori N;
 XX WPI; 2002-075313/10.
 XX N-PSDB; AAS99473.
 XX
 XX New human monoclonal antibody that binds to activation inducible
 PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid
 PT arthritis, multiple sclerosis and inflammation
 XX
 XX Claim 30; Page 270-271; 300pp; English.
 XX
 CC The invention relates to a novel human antibody (I), preferably a human
 CC monoclonal antibody which binds to an activation inducible lymphocyte
 CC immunomodulatory molecule (Ailim). (I) is useful for modulating signal
 CC transduction into a cell mediated by Ailim, for modulating proliferation
 CC of Ailim-expressing cells, for modulating production of a cytokine from
 CC Ailim-expressing cells, and for inducing antibody-dependent cytotoxicity
 CC against Ailim-expressing cells and/or immune cytotoxicity or apoptosis of
 CC Ailim-expressing cells. (I) is useful for treating, preventing or
 CC prophylaxis of delayed type allergy. (I) is useful for treating and
 CC preventing various diseases associated with Ailim-mediated
 CC costimulatory transduction, and for inhibiting the onset and/or
 CC advancement of the diseases. (I) is useful for suppression,
 CC prevention and/or treatment of rheumatoid arthritis, multiple
 CC sclerosis, autoimmune thyroiditis, allergic contact-type dermatitis,
 CC chronic inflammatory dermatosis, systemic lupus erythematosus, allergic
 CC insulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic
 CC disorders, inflammation, graft versus host reaction, graft versus host
 CC disease, immune rejection, disorders caused by abnormal intestinal
 CC immunity, specifically inflammatory intestinal disorders such as
 CC ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and
 CC pancreatitis. (I) induces no serious immunorejection due to antigenicity
 CC to human, i.e., human anti-mouse antiserum (HAMA) in a host.
 CC AAU74296-AAU74301 represent anti-human Ailim monoclonal antibody amino
 CC acid sequences of the invention.
 XX
 XX Sequence 236 AA;
 SQ
 Query Match 86.5%; Score 475; DB 23; Length 236;
 Best Local Similarity 88.7%; Pred. No. 1.4e-26;
 Matches 94; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

XX
 XX AA018424;
 AC
 XX 11-OCT-2002 (first entry)
 DT
 XX
 XX Anti-GD2 antibody light chain #1.
 DE
 XX
 XX Anti-GD2 antibody; neuroectodermal tumour; cancer; neuroblastoma;
 KM melanoma; vaccine; gene therapy; cytostatic; disialoganglioside GD2.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX DE10059930-A1.
 XX
 XX 29-MAY-2002.
 XX
 XX 23-NOV-2000; 2000DE-1059930.
 XX
 XX 23-NOV-2000; 2000DE-1059930.
 XX
 XX (FISC/) FISCHER P.
 XX (UTTE/) UTTEHREUTHER-FISCHER M.
 XX
 XX Uttenreuther-Fischer M, Krueger J;
 PI WPI; 2002-510006/55.
 XX
 XX Composition for treating tumors that produce disialoganglioside GD2,
 PT comprises human antibody fragment able to induce anti-idiotypic
 PT antibodies
 XX
 XX Claim 3; Fig 7A; 14pp; German.
 XX
 CC The present invention relates to a composition for treating tumors
 CC positive for disialoganglioside GD2 which is based on human antibody
 CC fragments that activate the immune system against GD2, specifically by
 CC inducing anti-GD2 antibodies. The composition can be used in the
 CC treatment of neuroblastoma and melanoma. The present sequence is an
 CC anti-GD2 antibody light chain.
 XX
 XX Sequence 105 AA;
 SQ
 Query Match 86.3%; Score 474; DB 23; Length 105;
 Best Local Similarity 89.5%; Pred. No. 8.2e-27;
 Matches 94; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTOSPSVSASVGDRTYITTCRASQGISWLAHYQHOGKAPKLLIYASASSLQSGVPSRF 60
 DB 25 QMTOSPPSSVSASVGDRTYITTCRASQGISWLAHYQHOGKAPKLLIYASASSLQSGVPSRF 84
 QY 61 SSGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFGQGTVEIKR 106
 DB 85 SSGSGYGTDFSLTISLQFEDSATYCCOANSFPYTFGQGTVEIKR 130

RESULT 9
 AAB72880
 ID AAB72880 standard; Protein; 107 AA.
 AC AAB72880;
 XX
 XX 10-MAY-2001 (first entry)
 DT
 XX
 XX Human anti-HER2/neu antibody 3-F2 light chain.
 DE
 XX
 XX Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy;
 KM 3-F2; 1-D2; 2-E8; growth factor receptor.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200109187-A2.

PD 08-FEB-2001.
 XX
 PF 25-JUL-2000; 2000MO-US20272.
 XX
 PR 29-JUL-1999; 99US-0146313.
 XX
 PR 10-MAR-2000; 2000US-0188539.
 XX
 PA (MEDA-) MEDAREX INC.
 XX
 PI Keler T, Deo Y;
 DR WPI; 2001-168698/17.
 DR N-PSDB; AAF75586.
 XX
 PT New human monoclonal antibody that specifically binds to growth factor
 PT receptor HER2/neu, for treating, preventing or diagnosing diseases
 XX characterized by aberrant HER2/neu expression e.g. cancers
 XX
 PS Disclosure; Page 104-105; 113pp; English.
 XX
 CC The present invention provides the protein and coding sequences for human
 CC monoclonal antibodies which bind specifically to the HER2/neu growth
 CC factor receptor (also known as erbB2). These are designated 3-F2, 1-D2
 CC and 2-E8. They can be used in the immunotherapy-based treatment and
 CC prognosis of cancers, particularly adenocarcinomas such as salivary
 CC gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas,
 CC and ovarian cancer. The present sequence is part of an antibody of the
 CC invention.
 CC
 SQ Sequence 107 AA;
 XX
 QY Query Match 85.1%; Score 467; DB 22; Length 107;
 Db Best Local Similarity 85.7%; Pred. No. 2.5e-26;
 Matches 90; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ELTQSPSSVSASVGRVITTCRASQGISWLAHYOHQPKAPKLLIYASASLSQGVPSRF 60
 Db 3 QMTQSPSSLSASVGRVITTCRASQGISWLAHYOHQPKAPKSLIYASASLSQGVPSRF 62
 QY 61 SSGSGYTDPSLTLSLQFEDSATYTCQANSFPYTGQGTKEIK 105
 Db 63 SSGSGYTDPSLTLSLQFEDSATYTCQANSFPYTGQGTKEIK 107
 Db
 RESULT 10
 AAUT6522
 ID AAUT6522 standard; Protein; 108 AA.
 XX
 AC AAUT6522;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Anti-interleukin-12 (IL-12) antibody variable region #2.
 XX
 KW Human; antibody; anti-interleukin-12; CDR; heavy chain; circulatory;
 KW complementarity determining region; neuroprotective; antiproliferative;
 KW immunosuppressant; cytostatic; anti-microbial; psoriasis; infection;
 KW multiple sclerosis; immune disorder; cardiovascular; malignant disease;
 KW neurological disorder.
 XX
 OS Homo sapiens.
 OS
 PN WO200212500-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 07-AUG-2001; 2001MO-US24720.
 XX
 PR 07-AUG-2000; 2000US-223358P.
 PR 29-SEP-2000; 2000US-236827P.
 PR 01-AUG-2001; 2001US-0920262.
 XX
 PA (CENZ) CENTOCOR INC.
 XX

XX
 PI Gilee-Komar J, Knight DM, Peritt D, Scallion B, Shealy D;
 XX
 DR WPI; 2002-257482/30.
 XX
 PT New mammalian anti-IL-12 antibodies, useful for diagnosing or treating
 PT IL-12 related conditions, e.g. psoriasis or multiple sclerosis, as well
 PT as other for treating immune, infectious, malignant or neurological
 PT disorders
 XX
 PS Claim 1; Page 93-94; 96pp; English.
 XX
 CC The invention relates to novel isolated mammalian anti-interleukin-12
 CC (IL-12) antibodies. The antibodies comprise at least one complementarity
 CC determining region (CDR) of a heavy or light chain, a heavy chain or
 CC light chain variable region, or a heavy chain or light chain constant
 CC region. The anti-IL-12 antibodies are useful in methods for diagnosing or
 CC treating IL-12 related conditions, e.g. psoriasis or multiple sclerosis.
 CC The antibodies are also useful for treating immune, cardiovascular,
 CC infectious, malignant or neurological disorders or diseases. The present
 CC sequence represents the amino acid sequence of human anti-interleukin-
 CC 12 (IL-12) antibody variable region #2.
 CC
 SQ Sequence 108 AA;
 XX
 QY Query Match 84.9%; Score 466; DB 23; Length 108;
 Db Best Local Similarity 84.9%; Pred. No. 3.1e-26;
 Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
 QY 1 ELTQSPSSVSASVGRVITTCRASQGISWLAHYOHQPKAPKLLIYASASLSQGVPSRF 60
 Db 3 QMTQSPSSLSASVGRVITTCRASQGISWLAHYOHQPKAPKSLIYASASLSQGVPSRF 62
 QY 61 SSGSGYTDPSLTLSLQFEDSATYTCQANSFPYTGQGTKEIK 106
 Db 63 SSGSGYTDPSLTLSLQFEDSATYTCQANSFPYTGQGTKEIK 108
 Db
 RESULT 11
 AAE10815
 ID AAE10815 standard; Protein; 109 AA.
 XX
 AC AAE10815;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human antibody CAT-212 light chain variable domain.
 XX
 KW Human; eotaxin; CAT-212; antibody; light chain variable region; VL;
 KW eczema; asthma; atopic disease; dermatological; rhinitis; food allergy;
 KW vasotropic; conjunctivitis; allergic colitis; psoriasis; pemphigoid;
 KW eosinophil-mediated disease; cellulitis; drug eruption; vasculitis;
 KW inflammatory bowel disease; gastroenteritis.
 XX
 OS Homo sapiens.
 OS
 PN WO200166754-A1.
 XX
 PD 13-SEP-2001.
 XX
 PF 02-MAR-2001; 2001MO-GB00927.
 XX
 PR 03-MAR-2000; 2000US-187246P.
 XX
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA Vaughan TJ, Walton AJ, Smith S;
 PI
 DR WPI; 2001-589944/66.
 XX

DR N-PSDB; AAD18149.
 XX
 PT Human antibodies against ectaxin useful for treating asthma, eczema and
 XX other atopic diseases, comprises an antibody variable heavy or variable
 PT light domain from CAT-212 or from complementary determining regions -
 XX
 PS Claim 1, Page 102; 107pp; English.
 CC The invention relates to a specific binding member which binds to human
 CC ectaxin. The binding member comprises an antibody variable heavy
 CC (VH)/variable light (VL) domain from CAT-212 VH/VL domain and a VH/VL
 CC domain comprising one or more VH/VL complementary determining regions
 CC (CDRs). Ectaxin is a chemottractant protein that binds to a specific
 CC receptor which is expressed predominantly on eosinophils. The binding
 CC member is useful for neutralising ectaxin, which is useful in treating
 CC asthma, eczema and other atopic diseases such as rhinitis, food allergy,
 CC conjunctivitis, allergic colitis which are recognised as eosinophil-
 CC mediated diseases; for treating skin and other atopic conditions such as
 CC psoriasis, pemphigoid, warts, syndrome, cellulitis, drug eruptions;
 CC inflammatory bowel disease which includes eosinophilic colitis/enteritis/
 CC gastroenteritis/Shulman's syndrome; vasculitis including Hughes-Stovin
 CC syndrome, Churg-Strauss syndrome. The present sequence is human
 CC antibody CAT-212 light chain variable domain (VL) which binds to ectaxin.
 CC
 SQ Sequence 109 AA;
 Query Match 84.6%; Score 464.5; DB 22; Length 109;
 Best Local Similarity 86.0%; Pred. No. 4e-26;
 Matches 92; Conservative 8; Mismatches 6; Indels 1; Gaps 1;
 QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISISMLAWYOHQPKAPKLIIYASSLSQGVPSRF 60
 DB 3 QNTQSPSSVSASVGDVITTCRASQDISISMLAWYQOKPKAPKLIIYASSLSQGVPSRF 62
 QY 61 SSGSGYGTDFSLTISLQPEDSATYVYCOQANSFP-YTFGGGTKEIKR 106
 DB 63 SSGSGGTDFTLTISLQPEDPATYVYCOQANSFPSTFGGTTLEIKR 109

RESULT 12
 AAG33597
 ID AAG33597 standard; Protein; 107 AA.
 AC AAG33597;
 XX
 DT 14-SEP-2001 (first entry)
 XX
 DE Human anti-Rh(D) chain I09 protein sequence.
 XX
 DE Human anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic.
 XX
 OS Homo sapiens.
 XX
 PN US6255455-B1.
 PD 03-JUL-2001.
 PF 29-JAN-1999; 99US-0240274.
 XX
 PR 11-OCT-1996; 96US-0028650.
 PR 10-APR-1998; 98US-0081380.
 PR 27-JUN-1997; 97US-0884045.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 PI Siegel DL;
 DR WPI; 2001-38931/41.
 DR N-PSDB; AAG68654.
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in

PT therapeutic medicine -
 XX
 PS Claim 1; Column 44; 162pp; English.
 XX
 CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG33558 to AAG33669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAG68615 to AAG68726 represent the nucleotide sequence which encode
 CC AAG33558 to AAG33669. AAG33670 to AAG33697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.
 CC
 SQ Sequence 107 AA;
 Query Match 84.3%; Score 463; DB 22; Length 107;
 Best Local Similarity 85.8%; Pred. No. 5e-26; Indels 0; Gaps 0;
 Matches 91; Conservative 7; Mismatches 8;
 QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISISMLAWYOHQPKAPKLIIYASSLSQGVPSRF 60
 DB 2 ELTQSPSSVSASVGDRTVITTCRASQGISISMLAWYQOKPKAPKLIIYASSLSQGVPSRF 61
 QY 61 SSGSGYGTDFSLTISLQPEDSATYVYCOQANSFPYTFGGGTKEIKR 106
 DB 62 SSGSGGTDFTLTISLQPEDPATYVYCOQANSFPYTFGGGTKEIKR 107

RESULT 13
 AAB72882
 ID AAB72882 standard; Protein; 107 AA.
 AC AAB72882;
 XX
 DT 10-MAY-2001 (first entry)
 XX
 DE Human anti-HER2/neu antibody 1-D2 light chain.
 XX
 DE Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy;
 KW 3-F2; 1-D2; 2-E8; growth factor receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO200109187-A2.
 PD 08-FEB-2001.
 PF 25-JUL-2000; 2000WO-US20272.
 XX
 PR 29-JUL-1999; 99US-0146313.
 PR 10-MAR-2000; 2000US-0188539.
 XX
 PA (MEDA-) MEDAREX INC.
 PI Keller T, Deo Y;
 DR WPI; 2001-168698/17.
 DR N-PSDB; AAF75588.
 PT New human monoclonal antibody that specifically binds to growth factor
 PT receptor HER2/neu, for treating, preventing or diagnosing diseases
 PT characterized by aberrant HER2/neu expression e.g. cancers -
 XX
 PS Disclosure; Page 107; 113pp; English.
 XX
 CC The present invention provides the protein and coding sequences for human
 CC monoclonal antibodies which bind specifically to the HER2/neu growth
 CC factor receptor (also known as erbB2). These are designated 3-F2, 1-D2
 CC and 2-E8. They can be used in the immunotherapy-based treatment and
 CC prognosis of cancers, particularly adenocarcinomas such as salivary

CC Blue cells were transformed with the library. Filamentous phage were

CC produced which expressed the MAb regions on their surface. Panning
 CC with gp120 and gp41 resulted in the recovery of immunoreactive
 CC clones. The light chain VK region sequence AAR54260 neutralises HIV1
 CC gp120.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 107 AA;

Query Match 83.8%; Score 460; DB 15; Length 107;
 Best Local Similarity 85.8%; Pred. No. 8.2e-26;
 Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

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 DB 1 ELTOSPPSSLSASVGDRTTTCRASQGISWLAWOHOPKAPKLIYSASSLSQGVPSRF 60
 QY 61 SSGSGYTDFTLTISSLOFEDSATYCCQANSPFPTFGGQTKVEIKR 106
 DB 61 SSGSGYTDFTLTISSLOFEDSATYCCQANSPFPTFGGQTKVEIKR 106

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	549	100.0	106	US-10-027-725A-12	Sequence 12, Appl
2	482	87.8	107	US-10-309-762-159	Sequence 159, App
3	479	87.2	107	US-10-309-762-62	Sequence 62, Appl
4	479	87.2	107	US-10-309-762-164	Sequence 164, Appl
5	478	87.1	107	US-10-309-762-61	Sequence 61, Appl
6	478	87.1	107	US-10-309-762-64	Sequence 64, Appl
7	478	87.1	244	US-09-880-748-1881	Sequence 1881, Ap
8	475	86.5	236	US-09-859-053-30	Sequence 30, Appl
9	474	86.3	107	US-10-041-860-43	Sequence 43, Appl
10	474	86.3	107	US-10-041-860-218	Sequence 218, App
11	473.5	86.2	106	US-10-309-762-84	Sequence 84, Appl
12	472	86.0	107	US-10-309-762-60	Sequence 60, Appl
13	472	86.0	107	US-10-309-762-63	Sequence 63, Appl
14	468.5	85.3	108	US-10-041-860-357	Sequence 357, App
15	466	84.9	108	US-09-920-262A-8	Sequence 8, Appl

16	464.5	84.6	109	US-09-798-058-4	Sequence 4, Appl
17	464.5	84.6	109	US-10-220-418-4	Sequence 4, Appl
18	463	84.3	107	US-09-848-798-40	Sequence 40, Appl
19	462.5	84.2	106	US-10-040-244-17	Sequence 17, Appl
20	462	84.2	106	US-10-027-725A-10	Sequence 10, Appl
21	460	83.8	107	US-10-016-986-104	Sequence 104, Appl
22	460	83.8	108	US-09-056-160B-12	Sequence 12, Appl
23	460	83.8	108	US-10-234-671-12	Sequence 12, Appl
24	460	83.8	108	US-09-795-798-3	Sequence 3, Appl
25	460	83.8	109	US-09-811-123-6	Sequence 6, Appl
26	460	83.8	110	US-10-044-896-4	Sequence 4, Appl
27	458	83.4	212	US-10-320-231A-77	Sequence 77, Appl
28	457	83.2	107	US-09-848-798-175	Sequence 175, Appl
29	457	83.2	107	US-09-848-798-176	Sequence 176, Appl
30	457	83.2	107	US-10-016-986-84	Sequence 84, Appl
31	457	83.2	107	US-10-091-300-33	Sequence 33, Appl
32	456	83.1	107	US-09-848-798-156	Sequence 156, Appl
33	455.5	83.0	106	US-10-309-762-85	Sequence 85, Appl
34	455.5	83.0	126	US-10-309-762-97	Sequence 97, Appl
35	455	82.9	107	US-10-608-626-5	Sequence 5, Appl
36	455	82.9	107	US-10-258-601-5	Sequence 5, Appl
37	454	82.7	108	US-10-025-687-8	Sequence 8, Appl
38	454	82.7	108	US-10-125-687-8	Sequence 8, Appl
39	454	82.7	244	US-09-880-748-82	Sequence 82, Appl
40	454	82.7	244	US-09-880-748-261	Sequence 261, Appl
41	453	82.5	237	US-09-880-748-1906	Sequence 1906, Ap
42	453	82.5	237	US-09-880-748-2003	Sequence 2003, Ap
43	453	82.5	237	US-09-880-748-2005	Sequence 2005, Ap
44	453	82.5	237	US-09-880-748-2017	Sequence 2017, Ap
45	453	82.5	237	US-09-880-748-2019	Sequence 2019, Ap

ALIGNMENTS

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RESULT 1
US-10-027-725A-12
; Sequence 12, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific Ige-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-12

Query Match      100.0%; Score 549; DB 15; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.8e-42;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ELTQSPSSVSASVGDRTVITTCASQGISWLAAYOHQPKAPKLIYASLSQGVPSRF 60
      |||
DB      1 ELTQSPSSVSASVGDRTVITTCASQGISWLAAYOHQPKAPKLIYASLSQGVPSRF 60
QY      61 SSGSGVGTDFSLTISLSQFEDSATYCYQQANSFPTFGGTVEIKR 106
      |||
DB      61 SSGSGVGTDFSLTISLSQFEDSATYCYQQANSFPTFGGTVEIKR 106

RESULT 2
US-10-309-762-159
; Sequence 159, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-159
```

```

Query Match      87.8%; Score 482; DB 12; Length 107;
Best Local Similarity 88.6%; Pred. No. 4e-36; Indels 0; Gaps 0;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
```

```

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLMAYOHQPKAPKLLIYSASLSQGVPSRF 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLMAYOQPKAPKLLIYAASLSQGVPSRF 62
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 61 SSGSGYGTDFSLTITSSIQFEDSATYTCQANSFPYTFGQGTKEIK 105
   |||||
DB 63 SSGSGGTDFTLTITSSIQPEDFATYTCQANSFPITFGQGTKEIK 107
   |||||
```

```

RESULT 3
US-10-309-762-62
; Sequence 62, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-62
```

```

US-10-309-762-62
```

```

Query Match      87.2%; Score 479; DB 12; Length 107;
Best Local Similarity 88.6%; Pred. No. 7.4e-36; Indels 0; Gaps 0;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
```

```

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLMAYOHQPKAPKLLIYSASLSQGVPSRF 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLMAYOQPKAPKLLIYAASLSQGVPSRF 62
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 61 SSGSGYGTDFSLTITSSIQFEDSATYTCQANSFPYTFGQGTKEIK 105
   |||||
DB 63 SSGSGGTDFTLTITSSIQPEDFATYTCQANSFPITFGQGTKEIK 107
   |||||
```

```

RESULT 4
US-10-309-762-164
; Sequence 164, Application US/10309762
; Publication No. US20040018198A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-164
```

```

Query Match      87.2%; Score 479; DB 12; Length 107;
Best Local Similarity 88.6%; Pred. No. 7.4e-36; Indels 0; Gaps 0;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
```

```

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLMAYOHQPKAPKLLIYSASLSQGVPSRF 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLMAYOQPKAPKLLIYAASLSQGVPSRF 62
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 61 SSGSGYGTDFSLTITSSIQFEDSATYTCQANSFPYTFGQGTKEIK 105
   |||||
DB 63 SSGSGGTDFTLTITSSIQPEDFATYTCQANSFPITFGQGTKEIK 107
   |||||
```

```

RESULT 5
US-10-309-762-61
; Sequence 61, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-61
```

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US-10-309-762-61
```

```

Query Match      87.1%; Score 478; DB 12; Length 107;
Best Local Similarity 87.6%; Pred. No. 9.1e-36; Indels 0; Gaps 0;
Matches 92; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
```

```

QY 1 ELTQSPSSVSASVGDRTVITTCRASQGISWLMAYOHQPKAPKLLIYSASLSQGVPSRF 60
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 3 QMTQSPSSVSASVGDRTVITTCRASQGISWLMAYOQPKAPKLLIYAASLSQGVPSRF 62
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
QY 61 SSGSGYGTDFSLTITSSIQFEDSATYTCQANSFPYTFGQGTKEIK 105
   |||||
DB 63 SSGSGGTDFTLTITSSIQPEDFATYTCQANSFPITFGQGTKEIK 107
   |||||
```

```

RESULT 6
US-10-309-762-64
; Sequence 64, Application US/10309762
```

Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Folitz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 64
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-64

Query Match 87.1%; Score 478; DB 12; Length 107;
Best Local Similarity 87.6%; Pred. No. 9,1e-36;
Matches 92; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTOSPSVSASVGDRTVITTCRASQGISSWLAWYQHOGKAPKLLIYASASSLQSGVPSRF 60
DB 3 QMTOSPSVSASVGDRTVITTCRASQGISSWLAWYQHOGKAPKLLIYASASSLQSGVPSRF 62

QY 61 SGSAGTDFSLTISLQFEDSATYCCOANSFPYFGGKTVEIKR 105
DB 63 SGSAGTDFSLTISLQFEDPATYCCOANSFPITFGGKTVEIKR 107

RESULT 7
US-09-880-748-1881
Sequence 1881, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1881
LENGTH: 244
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1881

Query Match 87.1%; Score 478; DB 11; Length 244;
Best Local Similarity 88.6%; Pred. No. 2,1e-35;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 LTGSSSVASVGDVTTTCRASQGISSWLAWYQHOGKAPKLLIYASASSLQSGVPSRF 61
DB 140 MTGSSSTLSASVGDVTTTCRASQGISSWLAWYQHOGKAPKLLIYASASSLQSGVPSRF 199

QY 62 GSGYTDLSLITSLQFEDSATYCCOANSFPYFGGKTVEIKR 106
DB 200 GSGGTDFTLITSLQFEDPATYCCOANSFPITFGGKTVEIKR 244

RESULT 8
US-09-859-053-30
Sequence 30, Application US/09859053
Patent No. US20020102658A1
GENERAL INFORMATION:
APPLICANT: Tezuka, Takashi
APPLICANT: Hori, No. US20020102658A1
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-053-30

Query Match 86.5%; Score 475; DB 10; Length 236;
Best Local Similarity 88.7%; Pred. No. 3,7e-35;
Matches 94; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTOSPSVSASVGDRTVITTCRASQGISSWLAWYQHOGKAPKLLIYASASSLQSGVPSRF 60
DB 25 QMTOSPSVSASVGDRTVITTCRASQGISRLAWYQHOGKAPKLLIYASASSLQSGVPSRF 84

QY 61 SGSAGTDFSLTISLQFEDSATYCCOANSFPYFGGKTVEIKR 106
DB 85 SGSAGTDFSLTISLQFEDPATYCCOANSFPITFGGKTVEIKR 130

RESULT 9
US-10-041-860-43
Sequence 43, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 43
LENGTH: 107
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-43

Query Match 86.3%; Score 474; DB 12; Length 107;
Best Local Similarity 87.6%; Pred. No. 2,1e-35;
Matches 92; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTOSPSVSASVGDRTVITTCRASQGISSWLAWYQHOGKAPKLLIYASASSLQSGVPSRF 60
DB 140 MTGSSSTLSASVGDVTTTCRASQGISSWLAWYQHOGKAPKLLIYASASSLQSGVPSRF 199

```

Oy      ELTQSPSSVNASVGDEVTITTCRASOGSISSMLAMWOHPKAKPLIIVYSSLSQGVPSPRF 60
       :|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db      3 QMTQSSTSSVASGVDNVTITTCRASOGSISSMLAMWQOKPKAKRLIIYAASSLQSGVPSRF 62
       :|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||

Oy      61 SSGSGGTDPSSLTISLQFEDSATYYYCOQANSEPYTFGGCTKVEIK 105
       :|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Db      63 SSGSGGTDFTLTITSLQPEDFATYYCOQANSF-WFGCGCTKVEIK 106
       :|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||

RESULT 12
Sequence 60, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudus, Jean
APPLICANT: Poltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: ABGENIX, 027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIORITY APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 60
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
```

```

Query Match      86.0%; Score 472; DB 12; Length 107;
Best Local Similarity   86.7%; Pred. No. 3, 1e-35;
Matches          91; Conservative    7; Mismatches    7; Indels    0; Gaps

QY      1 ELTQSPSSVASVGDENVITTCRASGCISSMLAMYOHQPKAKLLIYASASSIQGVPSRF 60
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      3 QMOWSPSSVASVGDDVVITTCRASGCGISIMLTWYQOKPKAKRLLIYASASSIQGVPSRF 62

QY      61 SGSGGYGDPFLTITSSLOPEDSATYYCOQANSFPFYTGOSTKYEIK 105
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      63 SGSGSGTDFTLTTISSLOPEDFATYYCOQANSFPFITGGOTRLEIK 107

RESULT 13
US-10-309-762-63
: Sequence 63, Application US/10309762
: Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudasz, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX 027A
CURRENT APPLICATION NUMBER: US/10/0309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 63
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens

```

Query Match	86.0%;	Score 472;	DB 12;	Length 107,
Best Local Similarity	86.7%;	Pred. No. 3.1e-35;		

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